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October 20, 2000

Box Patent Application

Commissioner for Patents
Washington, D.C. 20231

Re: U.S. Non-Provisional Utility Patent Application
Application No.: To Be Assigned
Filed: Herewith
For: Plant Polymorphic Markers and Uses Thereof
Inventors: David F. BUSH *et al.*
Atty. Docket: 04983.0206.CPUS01/38-21(15493)C

Sir:

The following documents are forwarded herewith for appropriate action by the U.S. Patent and Trademark Office:

1. Utility Patent Application Transmittal (PTO/SB/05);

2. U.S. Utility Patent Application entitled:

   Plant Polymorphic Markers and Uses Thereof

   and naming as inventors:

   David F. BUSH, Steven D. ROUNSLEY, and Roger C. WIEGAND

   the application consisting of:

   a. A specification containing:

      (i) 181 pages of a description prior to the claims;

      (ii) 6 page of claims (26 claims); and

      (iii) a one (1) page abstract;

3. Three (3) CD-ROMs containing the sequence listing; and

4. Two (2) return postcards.

This application is being filed without an executed Declaration, and without payment of official fees.

Submitted herewith are a sequence listing on CD-ROM (two copies) and a sequence listing Computer Readable Form (CRF) on CD-ROM, in compliance with 37 C.F.R. §§ 1.52(e), 1.77, AND 1.823 (AS AMENDED IN 65 Fed. Reg. 54603). It is Applicants' understanding that the U.S. Patent and Trademark Office is currently accepting sequence listing submissions in the format prescribed by the amended Code of Federal Regulations, although the new rules do not become mandatory until November 7, 2000.

Three CD-ROMs accompany this transmittal letter: two copies of a sequence listing (Copy 1 and Copy 2) and a sequence listing CRF. Copy 1 and Copy 2 of the sequence listing are identical to each other and to the sequence listing CRF. All three CD-ROMs each contain one file called "Marker Report.rpt" which is 13,491 kilobytes in size and was created on October 19, 2000. These CD-ROMs are IBM-PC machine format, and are MS-DOS and MS-Windows compatible.

It is respectfully requested that, of the two attached postcards, one be stamped with the filing date of these documents and returned to our courier, and the other, prepaid postcard, be stamped with the filing date and unofficial application number and returned as soon as possible.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)
June E. Cohan (Reg. No. 43,741)

Enclosures

PTO/SB/05 (2/98)

Please type a plus sign (+) inside this box → [+]

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Patent and Trademark Office: U.S. DEPARTMENT OF COMMERCE

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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	04983.0206.CPUS01
First Named Inventor or Application Identifier	BUSH
Title	Plant Polymorphic Markers and Uses Thereof
Express Mail Label No.	

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents

ADDRESS TO: Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

1. [ ] *Fee Transmittal Form (Form PTO-1082)
(Submit an original and a duplicate for fee processing)

2. [X] Specification [*Total Pages* 188]
(preferred arrangement set forth below)
- Descriptive title of the Invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R&D
- Reference to Microfiche Appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the Drawings (if filed)
- Detailed Description
- Claims
- Abstract of the Disclosure

3. [ ] Drawing(s) *(35 USC 113)* [*Total Sheets*]

4. Oath or Declaration [*Total Pages*]
a. [ ] Newly executed (original or copy)
b. [ ] Copy from a prior application (37 CFR 1.63(d))
(for continuation/divisional with Box 17 completed)
[Note Box 5 below]
i. [ ] DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

5. [ ] Incorporation By Reference *(useable if Box 4b is checked)*
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. [ ] Microfiche Computer Program *(Appendix)*

7. Nucleotide and/or Amino Acid Sequence Submission
(if applicable, all necessary)
a. [X] Computer Readable Copy
b. [ ] Paper Copy (identical to computer copy)
c. [ ] Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

8. [ ] Assignment Papers (cover sheet & document(s))
9. [ ] 37 CFR 3.73(b) Statement *(when there is an assignee)* [ ] Power of Attorney
10. [ ] English Translation Document *(if applicable)*
11. [ ] Information Disclosure Statement (IDS)/PTO-1449 [ ] Copies of IDS Citations
12. [ ] Preliminary Amendment
13. [X] Return Receipt Postcard (MPEP 503) (Two)
(should be specifically itemized)
14. [ ] *Small Entity Statement(s) [ ] Statement filed in prior application, Status still proper and desired
15. [ ] Certified Copy of Priority Document(s)
(if foreign priority is claimed)
16. [X] Other: 2 additional CD-ROMs containing Copy 1 and Copy 2 of sequence listing

*NOTE FOR ITEMS 1 & 14 IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C F R § 1 27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C.F R. § 1 28)

17. **If a CONTINUING APPLICATION**, *check appropriate box and supply the requisite information:*
[ ] Continuation [ ] Divisional [ ] Continuation-in-part (CIP) of prior application No: /
Prior Application Information: Examiner: Group/Art Unit:

18. CORRESPONDENCE ADDRESS

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Signature		*Date*	*October 20, 2000*

Burden Hour Statement This form is estimated to take 0.2 hours to complete Time will vary depending upon the needs of the individual case Any comments on the amount of time you are required to complete this form should be sent to the Chief Information Officer, Patent and Trademark Office, Washington, DC 20231 DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS SEND TO Assistant Commissioner for Patents, Box Patent Application, Washington, DC 20231

PLANT POLYMORPHIC MARKERS AND USES THEREOF

FIELD OF THE INVENTION

The present invention is in the field of plant genetics. More specifically, the invention relates to nucleic acid markers associated with *Arabidopsis thaliana* ecotypes. The invention also relates to methods for detecting polymorphisms.

INCORPORATION OF SEQUENCE LISTING

This application contains a sequence listing, which is contained on three identical CD-ROMs: two copies of a sequence listing (Copy 1 and Copy 2) and a sequence listing Computer Readable Form (CRF), all of which are herein incorporated by reference. All three CD-ROMs each contain one file called "Marker Report.rpt" which is 13,491 kilobytes in size and was created on October 19, 2000.

BACKGROUND OF THE INVENTION

I. *Arabidopsis thaliana*

The identification in *Arabidopsis thaliana* of polymorphic markers is important in the development of nutritionally enhanced or agriculturally enhanced crops. Such polymorphic markers are useful in, for example, genetic mapping or linkage analysis, marker assisted breeding, physical genome mapping, transgenic crop production, crop monitoring diagnostics, and gene identification and isolation.

Arabidopsis thaliana is widely used as a model organism for basic and applied research in the biology of flowering plants. *Arabidopsis thaliana* is a model system for plant genomic research in part due to its small and characterized genome, which is estimated to be comprised of approximately 20,000 to 25,000 genes. The genome is estimated to have a haploid content of around 100Mb, present on five chromosomes. Reported partial sequence analysis has provided information on genome features such as gene density and gene structure (Settles and Byrne, *Genome Research 8:*83-85 (1998), the

entirety of which is herein incorporated by reference). Based on reports from the European Union Sequencing Consortium, the average gene density is one gene every approximately 4.8kb.

Other important characteristics that make *Arabidopsis thaliana* a useful test system include its rapid life-cycle, small size, which allows for controlled growth in restricted space, its prolific seed production, the availability of characterized and uncharacterized mutants and the existence of a reliable transformation system.

Molecular genetics is often used in the analysis of plant genes and is particularly useful in the analysis of complex biological processes such as developmental regulation. In one approach the use of mutant plants, *e.g. Arabidopsis thaliana* mutants, in molecular genetic research requires the location of the mutation. Molecular markers are a useful way to locate such mutations.

Identification of target loci and the isolation of associated genes using molecular markers has been reported (Liu *et al.*, *Proc. Natl. Acad. Sci. USA*, *96*:6535-6540 (1999); Muramoto *et al.*, *The Plant Cell*, *11*:335-347 (1999); Bowman and Smyth, *Development*, *126*:2387-2396 (1999); Michaels and Amasino, *The Plant Cell*, *11*:949-956 (1999); Ha *et al.*, *The Plant Cell*, *11*:1153-1163 (1999); Walker *et al.*, *The Plant Cell*, *11*:1337-1349 (1999); Sedbrook *et al.*, *Proc. Natl. Acad. Sci. USA*, *96*:1140-1145 (1999); Kiyosue *et al.*, *Proc. Natl. Acad. Sci. USA*, *96*:4186-4191 (1999); and Davis *et al.*, *Proc. Natl. Acad. Sci. USA*, *96*:6541-6546 (1999), all of which are herein incorporated by reference in their entirety). The use of markers to isolate a genomic region of interest is often referred to as map based cloning, chromosome walking or positional cloning. Many of the *Arabidopsis thaliana* markers that have been used in map based cloning are anchored to genetic maps such as the Lister & Dean map (*See e.g.* http://genome-www3.stanford.edu/cgi-bin/AtDB/RIintromap).

Physical or partial physical maps of the *Arabidopsis thaliana* genome have also been reported (*See e.g.* http://genome-www3.stanford.edu/atdb_welcome.html). A

physical map of *Arabidopsis thaliana,* Columbia based on a collection of bacterial artificial chromosomes (BACs) is available (Marra *et al.*, *Nat. Genet.*, *22(3)*:265-270 (1999); Mozo *et al.*, *Nat. Genet.*, *22(e)*:271-275 (1999), both of which are herein incorporated by reference in their entirety). An overlapping series of BACs representing the *Arabidopsis thaliana,* Columbia genome is available from AIMS, Arabidopsis Biological Resource Center, 309 B&Z Building, 1735 Neil Avenue, Columbus, OH 43210, USA.

Cho *et al.* reported a low density biallelic polymorphic map based on a comparison of *Arabidopsis thaliana,* Columbia and *Arabidopsis thaliana,* Landsberg *erecta* ecotypes by screening approximately 0.5% of the genome for such polymorphisms (Cho *et al., Nature Genetics 23:*203-207 (1999), the entirety of which is herein incorporated by reference). In this survey 487 single nucleotide polymorphisms (SNPs) were reported. Cho *et al.* also reported the use of oligonucleotide arrays to detect *Arabidopsis thaliana* SNPs.

The present invention provides polymorphic nucleic acid markers whose physical location is known within the *Arabidopsis thaliana* genome. Moreover, the physical location of such markers is further known within a particular BAC and the position of that BAC relative to other BACs in the genome is also known.

Successful isolation of a region of *Arabidopsis thaliana* DNA associated with a trait of interest requires a nucleic acid marker to be sufficiently close to the trait. As the present invention provides a collection of nucleic acid markers in the *Arabidopsis thaliana* genome which allows for the efficient isolation of regions of *Arabidopsis thaliana* DNA associated with traits of interest. Moreover, the association of a collection of nucleic acid markers with a trait of interest may be simultaneously investigated.

Summary of the Invention

The present invention provides a collection of nucleic acid molecules capable of detecting a set of polymorphisms as shown in Table A.

The present invention also includes and provides a method of isolating a region of genomic DNA associated with a phenotype of interest comprising: (A) identifying an *Arabidopsis* plant having a first ecotype with the phenotype; (B) crossing the *Arabidopsis* plant with an *Arabidopsis* plant having a second ecotype lacking the phenotype of interest; (C) propagating and self pollinating seeds from the cross; (D) selecting progeny of self pollinated seeds with the phenotype of interest; (E) screening progeny of self pollinated seeds with the phenotype of interest with a collection of nucleic acid molecules, the collection of nucleic acid molecules capable of detecting a set of polymorphisms where the polymorphisms are distributed throughout the genome of the self pollinated seeds with the phenotype of interest at an average density of more than one polymorphism per about 100kb; (F) calculating the linkage of each of the nucleic acid molecules to the phenotype; and (G) isolating said region of genomic DNA associated with the phenotype based on its linkage to one or more of the nucleic acid molecules.

The present invention also provides a method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising: (A) screening a mapping population of *Arabidopsis* plants to determine the linkage of the phenotypic trait with a collection of nucleic acid molecules, wherein the nucleic acid molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of the mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb; (B) calculating the linkage of each of the nucleic acid molecules to the phenotypic trait; and (C) identifying the genomic DNA region associated the phenotypic trait based on its linkage to one or more of the nucleic acid molecules.

The present invention also provides a method of identifying a nucleic acid molecule associated with a phenotypic trait comprising: (A) screening a mapping population of *Arabidopsis* plants to determine the linkage of the phenotypic trait with polymorphisms, wherein the polymorphisms are distributed throughout the genome of the

mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb; (B) calculating the linkage of each of the polymorphism to the phenotypic trait; and (C) isolating the nucleic acid molecule associated with the phenotypic trait based on its linkage to one or more of the polymorphisms.

The present invention also provides a method of isolating a nucleic acid molecule associated with a phenotypic trait comprising: (A) screening a mapping population of *Arabidopsis* plants to determine the linkage of the phenotypic trait with a polymorphism, wherein the polymorphism is selected from the group consisting of a polymorphism from Table A; and (B) isolating the nucleic acid molecule associated with the phenotypic trait based on its linkage to one or more of the polymorphisms.

The present invention also provide a method of introgressing a trait of interest into a plant comprising using a nucleic acid marker for marker assisted selection of the plant, the nucleic acid marker capable of detecting a polymorphism selected from Table A, and introgressing the trait into said plant.

The present invention also provides a collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population, wherein the collection of non-identical nucleic acid molecules is capable of detecting at least 25 polymorphisms selected from the group consisting of Table A.

The present invention also provides a computer readable medium having recorded thereon at least 100 of the polymorphisms set forth in Table A.

The present invention also provides a method for identifying transposons in the DNA of an organism comprising identifying INDELs in that DNA and comparing the sequence of the INDELs to the sequence of one or more known transposons.

Detailed Description of the Invention

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem. 55*:831-854 (1986), the entirety of which is herein incorporated by reference). A "polymorphism" is a variation

or difference in the sequence of a genetic region that arises in some of the members of a species. Variant sequences can be defined with reference to an arbitrary or non-arbitrary standard sequence for the species. A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the "standard" sequence (*i.e.* the standard "allele") whereas other members may have a variant sequence (*i.e.*, a variant "allele"). Thus, as used herein, an allele is one of two or more alternative versions of a gene or other genetic region at a particular location on a chromosome. In the simplest case, only one variant sequence may exist, and the polymorphism is thus said to be bi-allelic. In other cases, the species' population may contain multiple alleles, and the polymorphism is termed tri-allelic, *etc.*

A single gene or genetic region may have multiple different unrelated polymorphisms. For example, it may have a one bi-allelic polymorphism at one site, another bi-allelic polymorphism at another site and a multi-allelic polymorphism at another site. When all the sequences for a group of alleles at a chromosomal locus in a plant are the same, the alleles are said to be "homozygous" at that locus. When the sequence of any allele at a particular locus in a plant is different, the population of alleles is said to be "heterozygous" at that locus.

Phenotypic traits can vary due to environmental and/or genetic factors. For example, polymorphisms at a particular chromosomal locus can affect the phenotypic trait associated with that locus.

As used herein, a phenotypic trait of interest may be any trait exhibited by a plant, whether naturally occurring or otherwise, that is capable of being inherited. Moreover, the phenotypic trait of interest may, for example, be transient, permanent or only present when the plant or part thereof is subjected to environmental stimuli or challenge. A phenotypic trait of interest may be a desired trait. In other cases the phenotypic trait of interest may be an undesired trait. Furthermore, phenotypic traits are not limited to visible traits. While the phenotypic trait may be any trait, preferred traits of interest are those

that have agricultural significance. Examples of agricultural traits include those that affect a component of yield, those that provide disease or chemical resistance, and those that affect developmental traits such as pollen or ovule production, *etc.*, and those that affect composition of plants or plant parts, including seed proteins or oils, starch or sugar composition, nutrient content and the like.

Many phenotypic traits are the result of multiple genes or genetic factors, for example, a phenotypic trait that is the result of a quantitative trait allele. An allele of a quantitative trait locus (QTL) can, of course, comprise multiple genes or other genetic factors even within a contiguous genomic region or linkage group. As used herein, an allele of a quantitative trait locus can therefore encompass more than one gene or other genetic factor where each individual gene or genetic component is also capable of exhibiting allelic variation and where each gene or genetic factor also has a phenotypic affect on the quantitative trait in question.

As used herein, a "marker" is an indicator for the presence of at least one polymorphism. A marker is preferably a nucleic acid molecule. It is understood that a marker can, for example, be an oligonucleotide probe or primer.

A "nucleic acid marker" as used herein means a nucleic acid molecule that is capable of being a marker for detecting a polymorphism.

The term "oligonucleotide" as used herein refers to short nucleic acid molecules useful, *e.g.* for hybridizing probes, nucleotide array elements or amplification primers. Oligonucleotide molecules are comprised of two or more nucleotides, *i.e.* deoxyribonucleotides or ribonucleotides, preferably more than five and up to 30 or more. The exact size will depend on many factors, which in turn depend on the ultimate function or use of the oligonucleotide. Oligonucleotides can comprise ligated natural nucleic molecules acids or synthesized nucleic acid molecules and comprise between 5 to 150 nucleotides or between about 15 and about 100 nucleotides, or preferably up to 100 nucleotides, and even more preferably between 15 to 30 nucleotides or most preferably

between 18-25 nucleotides, identical or complementary to a sequence of similar length. This invention provides oligonucleotides capable of detecting polymorphisms. Such oligonucleotides may be nucleic acid elements for use on solid arrays (*e.g.* synthesized or spotted). Such oligonucleotides may also be primers for use in polymerase chain reaction (PCR) or other reactions. The term "primer" as used herein refers to a nucleic acid molecule, preferably an oligonucleotide whether derived from a naturally occurring molecule such as one isolated from a restriction digest or one produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, *i.e.*, in the presence of nucleotides and an agent for polymerization such as DNA polymerase and at a suitable temperature and pH. The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the agent for polymerization. The exact lengths of the primers will depend on many factors, including temperature and source of primer. For example, depending on the complexity of the target sequence, the oligonucleotide primer typically contains at least 15, more preferably 18 nucleotides, which are identical or complementary to the template and optionally a tail of variable length which need not match the template. The length of the tail should not be so long that it interferes with the recognition of the template. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

The primers herein are selected to be "substantially" complementary to the different strands of each specific sequence to be amplified. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a

non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence of the strand to be amplified to hybridize therewith and thereby form a template for synthesis of the extension product of the other primer. Computer generated searches using programs such as Primer3 (www-genome.wi.mit.edu/cgi-bin/primer/primer3.cgi), STSPipeline (www-genome.wi.mit.edu/cgi-bin/www-STS_Pipeline), or GeneUp (Pesole *et al.*, *BioTechniques 25*:112-123 (1998), the entirety of which is herein incorporated by reference), for example, can be used to identify potential PCR primers. Exemplary primers include primers that are 18 to 50 bases long, where at least between 18 to 25 bases are identical or complementary to at least 18 to 25 bases of a segment of the template sequence.

This invention also contemplates and provides primer pairs for amplification of nucleic acid molecules in order to detect polymorphisms. As used herein "primer pair" means a set of two oligonucleotide primers based on two separated sequence segments of a target nucleic acid sequence. One primer of the pair is a "forward primer" or "5' primer" having a sequence which is identical to the more 5' of the separated sequence segments (+ strand). The other primer of the pair is a "reverse primer" or "3' primer" having a sequence which is complementary to the more 3' of the separated sequence segments (+ strand). A primer pair allows for amplification of the nucleic acid sequence between and including the separated sequence segments. Optionally, each primer pair can comprise additional sequences, *e.g.* universal primer sequences or restriction endonuclease sites, at the 5' end of each primer, *e.g.* to facilitate cloning, DNA sequencing, or reamplification of the target nucleic acid sequence.

As used herein, a "mapping population" is a collection of plants capable of being used with markers to map the genetic position of traits.

As used herein, a polymorphic marker is a marker capable of detecting one or more polymorphisms.

The present invention provides nucleic acid molecules which are markers, *i.e.* capable of detecting polymorphisms that are distributed throughout the genome of a mapping population.

As used herein, a "characterized polymorphism" is a polymorphism whose physical position on a genome is known. In a preferred embodiment, the physical position of a characterized polymorphism on an isolated nucleic acid molecule, such as a bacterial artificial chromosome comprising *Arabidopsis thaliana* genomic DNA, is known. Thus the present invention also provides nucleic acid molecules capable of detecting characterized polymorphisms throughout a genome.

In a further preferred embodiment, a characterized polymorphism is any polymorphism where the nucleic acid sequences of at least two of the polymorphisms present in an *Arabidopsis* mapping population are known (sequenced characterized polymorphism). In a particularly preferred embodiment, a characterized polymorphism is a polymorphism from Table A. In another particularly preferred embodiment, a characterized polymorphism from Table A is part of a collection of polymorphisms, where preferably over 25%, more preferably over 50% and even more preferably over 75% of the polymorphisms are selected from the polymorphisms in Table A.

The present invention provides nucleic acid molecules capable of detecting insertion/deletion polymorphisms (INDELs) in *Arabidopsis* at an average density of one INDEL per 8.4 kb. The present invention also provides nucleic acid molecules capable of detecting single nucleotide polymorphisms (SNPs) at an average density of one SNP per 3.9 kb. The present invention also provides nucleic acid molecules capable of detecting polymorphisms at an average density of one polymorphism per 2.7 kb.

As used herein, an "INDEL" is any insertion/deletion polymorphism characterized by additional nucleotides in at least one allele as compared to a reference allele. As used

herein, a "SNP" is any polymorphism characterized by a different single nucleotide at a particular physical position in at least one allele.

The polymorphisms capable of detection by nucleic acid molecules of the present invention are distributed throughout the genome of the mapping population in a manner that allows the efficient identification of a genomic region associated with a phenotypic trait. In a preferred embodiment, the polymorphisms are distributed throughout the genome where 60%, preferably 70%, more preferably 80%, even more preferably 90%, 95% or 100% of the genome has a characterized polymorphism at a density of higher than one polymorphism per 100kb, more preferably higher than one polymorphism per 50kb, and even more preferably higher than one polymorphism per 25kb, 10kb, 7kb, 5kb or 3kb. In another preferred embodiment, the polymorphisms are distributed throughout the genome where 60%, preferably 70%, more preferably 80%, even more preferably 90%, 95% or 100% of genome has a characterized polymorphism at a density of higher than one polymorphism per 3.5cM, more preferably higher than one polymorphism per 3.25cM, and even more preferably higher than one polymorphism per 3.0cM, 2.75cM, 2.5cM, 2.0cM, 1.5cM, 1.0cM or 0.5cM.

In a preferred embodiment of the present invention, the efficient identification of a genomic region associated with a phenotypic trait, *e.g.* a QTL or a single gene, is provided, where the genomic region is less than 100kb, more preferably less than 50kb, and even more preferably less than 25kb, 10kb, 7kb, 5kb or 3kb from a characterized polymorphism. In another preferred embodiment of the present invention the efficient identification of a genomic region associated with a phenotypic trait where the genomic region is less than 3.5cM, more preferably less than 3.25cM, and even more preferably less than 3cM, 2.75cM, 2.5cM, 2.0cM, 1.5cM, 1.0cM or 0.5cM from a characterized polymorphism.

It is understood that the distribution of polymorphisms need not be uniform in a genome as certain regions will exhibit a higher average density of polymorphisms (*e.g.*

non-centromeric regions) and certain regions will exhibit a lower average density of polymorphisms (*e.g.* centromeric regions).

In a preferred embodiment, the efficient identification of a genomic region associated with a phenotypic trait of interest will be obtained by a simultaneous screening for the presence of 25 or more, more preferably 50 or more, even more preferably 75 or more, 100 or more, 150 or more, 200 or more, 250 or more, 300 or more, 400 or more or 500 or more, 1,000 or more, 2,000 or more, 3,000 or more, 4,000 or more polymorphisms. In an even more preferred embodiment, the efficient identification of a genomic region associated with a phenotypic trait of interest will be obtained by a simultaneously screening for the presence of 25 or more, more preferably 50 or more, even more preferably (where appropriate) 100 or more, or 250 or more *etc.* of the polymorphisms in Table A.

In another preferred embodiment, the efficient identification of a genomic region associated with a phenotypic trait of interest will be obtained by screening for the presence of 25 or more, more preferably 50 or more, even more preferably 75 or more, 100 or more, 150 or more, 200 or more, 250 or more, 300 or more, 400 or more or 500 or more, 1,000 or more, 2,000 or more, 3,000 or more, 4,000 or more polymorphisms during a single assay. In an even more preferred embodiment the efficient identification of a genomic region associated with a phenotypic trait of interest will be obtained by screening for the presence of 25 or more, more preferably 50 or more, even more preferably (where appropriate) 100 or more or 250 or more *etc.* of the polymorphisms in Table A during a single assay. A single assay can comprise many steps. One or more of these steps can occur sequentially.

In an embodiment of the present invention, the assay is carried out using a high throughput system. A particularly preferred high throughput system involves a solid phase array. A particularly preferred solid phase array is a microarray.

In the assays below, a collection of markers for polymorphisms can comprise from a few up to millions of different nucleic acid molecules. For example, using simple dot-blot hybridization methods, membranes with many nucleic acid molecules can be generated for screening. The solid-phase techniques described below and known in the art can be adapted for high-throughput monitoring of polymorphisms. In such methods different immobilized nucleic acid molecule probes can be placed on a solid support at microarray densities of up to millions of nucleic acid molecules per square inch. Similarly, very large sets of nucleic acid molecules can be immobilized for simultaneous screening against one or more probes.

Several methods have been described for fabricating microarrays of nucleic acid molecules and using such microarrays in detecting nucleic acid sequences. For instance, microarrays of markers for polymorphisms can be fabricated by spotting nucleic acid molecules, *e.g.* oligonucleotides, onto substrates or fabricating oligonucleotide sequences *in situ* on a substrate. Spotted or fabricated nucleic acid molecules can be applied in a high density matrix pattern of up to about 30 non-identical nucleic acid molecules per square centimeter or higher, *e.g.* up to about 100 or even 1,000 per square centimeter or higher. Useful substrates for arrays include nylon, glass and silicon. See, for instance, 5,202,231; 5,242,974; 5,384,261; 5,405,783; 5,412,087; 5,424,186; 5,429,807; 5,436,327; 5,445,934; 5,472,672; 5,525,464; 5,527,681; 5,529,756; 5,532,128; 5,545,531; 5,554,501; 5,556,752; 5,561,071; 5,571,639; 5,593,839; 5,599,695; 5,624,711; 5,658,734; 5,700,637; 5,744,305; 5,800,992; 6,004,755 and 6,087,102 the disclosures of all of which are incorporated herein by reference in their entireties. Sequences can be efficiently analyzed by hybridization or primer extension. See, for instance, U.S. Patents 5,202,231; 5,445,934; 5,492,806; 5,525,464; 5,695,940; 5,700,637; 5,744,305; 5,800,992; 5,807,522; and 5,830,645, all of which are incorporated herein by reference in their entirety. Nucleic acid molecule microarrays may be screened with molecules or fragments thereof to determine nucleic acid molecules that specifically bind molecules or fragments thereof.

In a preferred embodiment, a microarray of the present invention comprises at least 10 nucleic acid molecules that specifically hybridize under high stringency to at least 10 polymorphic nucleic acid sequences characterized by this invention. In a more preferred embodiment, a microarray of the present invention comprises at least 100 nucleic acid molecules that specifically hybridize under high stringency to at least 100 characterized polymorphic nucleic acid sequences; more preferably at least 1,000 or 2,500 marker nucleic acid molecules that specifically hybridize under high stringency to at least 1,000 or 2,500 characterized polymorphic nucleic acid sequences; even more preferably at least at least 4,000 or more marker nucleic acid molecules that specifically hybridize under high stringency to at least 4,000 or more characterized polymorphic nucleic acid sequences.

In a preferred embodiment, a microarray of the present invention comprises at least 10 nucleic acid molecules capable of detecting or characterizing by primer extension to at least 10 polymorphic nucleic acid sequences characterized by this invention. In a more preferred embodiment, a microarray of the present invention comprises at least 100 nucleic acid molecules capable of detecting or characterizing by primer extension to at least 100 characterized polymorphic nucleic acid sequences; even more preferably at least 1,000 or 2,500 nucleic acid molecules capable of detecting or characterizing by primer extension to at least 1,000 or 2,500 characterized polymorphic nucleic acid sequences; even more preferably at least 4,000 or more nucleic acid molecules capable of detecting or characterizing by primer extension to at least 4,000 or more characterized polymorphic nucleic acid sequences.

In a preferred embodiment, the microarray is a variant detector array (VDA)(Cho *et al., Nature Genetics 23:*203-207 (1999); Wang *et al., Science 280:* 1077-1082 (1998), the entirety of which is herein incorporated by reference; Winzeler *et al., Curr. Opin. Genet. Dev. 4:* 602-608 (1997), the entirety of which is herein incorporated by reference). For example, each detection block can consist of four variant detector arrays (VDAs)

corresponding to the alternative alleles: two for the forward strand sequence and two for the reverse strand sequence (*See e.g.* Cho *et al., Nature Genetics 23:*203-207 (1999)). For each of the interrogated positions (for example, -5 to +5 relative to the polymorphic position), a set of four suitable length oligonucleotides per SNP or other polymorphism (*e.g.* 25-mers are prepared where the oligonucleotides are complementary to the SNP or other polymorphic region except at the interrogated position). Hybridization of the oligonucleotides with the matching allele results in a strong signal.

The detection or screening of polymorphic nucleic acid sites in a sample of DNA may be facilitated, for example, through including the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (*e.g.*, a Variable Number of Tandem Repeats (VNTR) polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs"). RFLPs have been widely used in human and plant genetic analyses (Glassberg, UK Patent Application 2135774; Skolnick *et al.*, *Cytogen. Cell Genet. 32*:58-67 (1982); Botstein *et al.*, *Ann. J. Hum. Genet. 32*:314-331 (1980); Fischer *et al.*, PCT Application WO 90/13668; Uhlen, PCT Application WO 90/11369, all of which are herein incorporated by reference in their entirety).

An alternative method of determining polymorphisms is based on cleaved amplified polymorphic sequences (CAPS) (Konieczny, A. and F.M. Ausubel, *Plant J.*

4:403-410 (1993); Lyamichev *et al.*, *Science 260*:778-783 (1993), the entireties of which are herein incorporated by reference). One advantage of this method is the large amount of target DNA that is generated by amplification which eliminates the requirement for radiolabeling for detection of the polymorphism.

Polymorphisms can also be identified by single strand conformation polymorphism (SSCP) analysis. The SSCP technique is a method capable of identifying most sequence variations in a single strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996), the entirety of which is herein incorporated by reference; Orita *et al., Genomics 5:*874-879 (1989), the entirety of which is herein incorporated by reference). Under denaturing conditions a single strand of DNA will adopt a conformation that is uniquely dependent on its sequence. This conformation usually will be different even if only a single base is changed. Most conformations have been reported to alter the physical configuration or size sufficiently to be detectable by electrophoresis. A number of protocols have been described for SSCP including, but not limited to Lee *et al., Anal. Biochem. 205:*289-293 (1992), the entirety of which is herein incorporated by reference; Suzuki *et al., Anal. Biochem. 192:*82-84 (1991), the entirety of which is herein incorporated by reference; Lo *et al., Nucleic Acids Research 20:*1005-1009 (1992), the entirety of which is herein incorporated by reference; Sarkar *et al., Genomics 13:*441-443 (1992), the entirety of which is herein incorporated by reference).

Polymorphisms may also be detected using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA. Vos *et al.*, *Nucleic Acids Res. 23*:4407-4414 (1995), the entirety of which is herein incorporated by reference. This method allows for the specific co-amplification of many restriction fragments, which can be analyzed without knowledge of the nucleic acid sequence. AFLP employs basically three steps. Initially, a sample of genomic DNA is

cut with restriction enzymes and oligonucleotide adapters are ligated to the restriction fragments of the DNA. The restriction fragments are then amplified using PCR by using the adapter and restriction sequence as target sites for primer annealing. The selective amplification is achieved by the use of primers that extend into the restriction fragments, amplifying only those fragments in which the primer extensions match the nucleotide flanking the restriction sites. These amplified fragments are then visualized on a denaturing polyacrylamide gel (Beismann *et al.*, *Mol. Ecol. 6*:989-993 (1997); Janssen *et al.*, *Int. J. Syst. Bacteriol 47*:1179-1187 (1997); Huys *et al.*, *Int. J. Syst. Bacteriol. 47*:1165-1171 (1997); McCouch *et al.*, *Plant Mol. Biol. 35*:89-99 (1997); Nandi *et al.*, *Mol. Gen. Genet. 255*:1-8 (1997); Cho *et al.*, *Genome 39*:373-378 (1996); Simons *et al.*, *Genomics 44*:61-70 (1997); Cnops *et al.*, *Mol. Gen. Genet. 253*:32-41 (1996); Thomas *et al.*, *Plant J. 8*:785-794 (1995), all of which are herein incorporated by reference in their entirety).

Polymorphisms may also be detected using random amplified polymorphic DNA (RAPD) (Williams *et al.*, *Nucl. Acids Res. 18*:6531-6535 (1990), the entirety of which is herein incorporated by reference).

SNPs generally occur at greater frequency than other polymorphic markers and are spaced with a greater uniformity throughout a genome than other reported forms of polymorphism. The greater frequency and uniformity of SNPs means that there is greater probability that such a polymorphism will be found near or in a genetic locus of interest than would be the case for other polymorphisms. SNPs are located in protein-coding regions and noncoding regions of a genome. Some of these SNPs may result in defective or variant protein expression (*e.g.*, as a result of mutations or defective splicing). Analysis (genotyping) of characterized SNPs can require only a plus/minus assay rather than a lengthy measurement, permitting easier automation.

SNPs can be characterized using any of a variety of methods. Such methods include the direct or indirect sequencing of the site, the use of restriction enzymes

(Botstein *et al.*, *Am. J. Hum. Genet. 32*:314-331 (1980), the entirety of which is herein incorporated reference; Konieczny and Ausubel, *Plant J. 4*:403-410 (1993), the entirety of which is herein incorporated by reference), enzymatic and chemical mismatch assays (Myers *et al.*, *Nature 313*:495-498 (1985), the entirety of which is herein incorporated by reference), allele-specific PCR (Newton *et al.*, *Nucl. Acids Res. 17*:2503-2516 (1989), the entirety of which is herein incorporated by reference; Wu *et al.*, *Proc. Natl. Acad. Sci. USA 86*:2757-2760 (1989), the entirety of which is herein incorporated by reference), ligase chain reaction (Barany, *Proc. Natl. Acad. Sci. USA 88*:189-193 (1991), the entirety of which is herein incorporated by reference), single-strand conformation polymorphism analysis (Labrune *et al.*, *Am. J. Hum. Genet. 48*: 1115-1120 (1991), the entirety of which is herein incorporated by reference), single base primer extension (Kuppuswamy *et al.*, *Proc. Natl. Acad. Sci. USA 88*:1143-1147 (1991), Goelet US 6,004,744; Goelet 5,888,819; all of which are herein incorporated by reference in their entirety), solid-phase ELISA-based oligonucleotide ligation assays (Nikiforov *et al.*, *Nucl. Acids Res. 22*:4167-4175 (1994), dideoxy fingerprinting (Sarkar *et al.*, *Genomics 13*:441-443 (1992), the entirety of which is herein incorporated by reference), oligonucleotide fluorescence-quenching assays (Livak *et al.*, *PCR Methods Appl. 4*:357-362 (1995a), the entirety of which is herein incorporated by reference), 5'-nuclease allele-specific hybridization TaqMan™ assay (Livak *et al.*, *Nature Genet. 9*:341-342 (1995), the entirety of which is herein incorporated by reference), template-directed dye-terminator incorporation (TDI) assay (Chen and Kwok, *Nucl. Acids Res. 25*:347-353 (1997), the entirety of which is herein incorporated by reference), allele-specific molecular beacon assay (Tyagi *et al.*, *Nature Biotech. 16*: 49-53 (1998), the entirety of which is herein incorporated by reference), PinPoint assay (Haff and Smirnov, *Genome Res. 7*: 378-388 (1997), the entirety of which is herein incorporated by reference), dCAPS analysis (Neff *et al.*, *Plant J. 14*:387-392 (1998), the entirety of which is herein incorporated by reference), pyrosequencing (Ronaghi *et al, Analytical Biochemistry 267*:65-71 (1999); Ronaghi *et al*

PCT application WO 98/13523; Nyren *et al* PCT application WO 98/28440, all of which are herein incorporated by reference in their entirety; http//www.pyrosequencing.com), using mass spectrometry *e.g.*, the Masscode ™ system (Howbert *et al* WO 99/05319; Howber *et al* WO 97/27331, all of which are herein incorporated by reference in their entirety; http//www.rapigene.com; Becker *et al* PCT application WO 98/26095; Becker *et al* PCT application; WO 98/12355; Becker *et al* PCT application WO 97/33000; Monforte *et al* US 5,965,363, all of which are herein incorporated by reference in their entirety), invasive cleavage of oligonucleotide probes (Lyamichev *et al Nature Biotechnology 17*:292-296, herein incorporated by reference in its entirety; http//www.twt.com), using high density oligonucleotide arrays (Hacia *et al Nature Genetics 22*:164-167; herein incorporated by reference in its entirety; http//www.affymetrix.com).

INDELs are identified by comparing sequence of *Arabidopsis thaliana* ecotypes Columbia and Landsberg erecta. Certain INDELs are believed to have resulted from insertion or excision of transposable elements. Thus, INDEL sequences can be used to identify candidate sequences for active transposons by comparing INDEL sequences to the sequence of known transposons. For instance, certain INDEL sequences of greater than 100 bp were found to exhibit similarity to the sequence of MuDR transposable element from maize.

Polymorphisms may also be detected using allele-specific oligonucleotides (ASO), which, can be for example, used in combination with hybridization based technology including southern, northern, and dot blot hybridizations, reverse dot blot hybridizations and hybridizations performed on microarray and related technology.

The stringency of hybridization for polymorphism detection is highly dependent upon a variety of factors, including length of the allele-specific oligonucleotide, sequence composition, degree of complementarity (*i.e.* presence or absence of base mismatches), concentration of salts and other factors such as formamide, and temperature. These

factors are important both during the hybridization itself and during subsequent washes performed to remove target polynucleotide that is not specifically hybridized. In practice, the conditions of the final, most stringent wash are most critical. In addition, the amount of target polynucleotide that is able to hybridize to the allele-specific oligonucleotide is also governed by such factors as the concentration of both the ASO and the target polynucleotide, the presence and concentration of factors that act to "tie up" water molecules, so as to effectively concentrate the reagents (*e.g.*, PEG, dextran, dextran sulfate, *etc.*), whether the nucleic acids are immobilized or in solution, and the duration of hybridization and washing steps.

Hybridizations are preferably performed below the melting temperature (T_m) of the ASO. The closer the hybridization and/or washing step is to the T_m, the higher the stringency. T_m for an oligonucleotide may be approximated, for example, according to the following formula: $T_m = 81.5 + 16.6 \times (\log10[Na+]) + 0.41 * (\%G+C) - 675/n$; where [Na+] is the molar salt concentration of Na+ or any other suitable cation and n = number of bases in the oligonucleotide. Other formulas for approximating T_m are available and are known to those of ordinary skill in the art.

Stringency is preferably adjusted so as to allow a given ASO to differentially hybridize to a target polynucleotide of the correct allele and a target polynucleotide of the incorrect allele. Preferably, there will be at least a two-fold differential between the signal produced by the ASO hybridizing to a target polynucleotide of the correct allele and the level of the signal produced by the ASO cross-hybridizing to a target polynucleotide of the incorrect allele (*e.g.*, an ASO specific for a mutant allele cross-hybridizing to a wild-type allele). In more preferred embodiments of the present invention, there is at least a five-fold signal differential. In highly preferred embodiments of the present invention, there is at least an order of magnitude signal differential between the ASO hybridizing to a target polynucleotide of the correct allele and the level of the

signal produced by the ASO cross-hybridizing to a target polynucleotide of the incorrect allele.

While certain methods for detecting polymorphisms are described herein, other detection methodologies may be utilized. For example, additional methodologies are known and set forth, in Birren *et al.*, *Genome Analysis,* 4:135-186, *A Laboratory Manual. Mapping Genomes*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1999); Maliga *et al.*, *Methods in Plant Molecular Biology. A Laboratory Course Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1995); Paterson, *Biotechnology Intelligence Unit: Genome Mapping in Plants*, R.G. Landes Co., Georgetown, TX, and Academic Press, San Diego, CA (1996); *The Maize Handbook*, Freeling and Walbot, eds., Springer-Verlag, New York, NY (1994); *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Elles, ed., Humana Press, Totowa, NJ (1996); Clark, ed., *Plant Molecular Biology: A Laboratory Manual*, Clark, ed., Springer-Verlag, Berlin, Germany (1997), all of which are herein incorporated by reference in their entirety.

Detection of one or more of the polymorphisms, preferably one or more of the characterized polymorphisms, may be carried out using a collection of nucleic acid markers.

Preferred aspects of this invention comprise collections of nucleic acid markers comprising nucleic acid molecules where the collections range in size from about 10 non-identical members or more, to at least about 100 or 270 or higher, more preferably at least about 300 or 350, most preferably at least 400 or 500 or higher, up to about 1,000, or 2000 or even higher, say about 4,000 or greater, or more non-identical members. As used herein a non-identical member is a member that differs in nucleic acid or amino acid sequence. For example, a non-identical nucleic acid molecule is a nucleic acid molecule that differs in nucleic acid sequence from the nucleic acid molecule to which it is being compared. For example a nucleic acid molecule having the sequence 5' CCC 3' is not

identical – *i.e.* is non-identical – to a nucleic acid molecule having the sequence 5' CCG 3'. In one limited aspect a collection may comprise all of the nucleic acid markers identified by this invention. Collections of nucleic acid markers can be located or organized in a variety of forms, *e.g.* on microarrays, in solutions, in bacterial clone libraries, *etc.* As used herein, an "organized" collection is a collection where the nucleic acid or amino acid sequence of a member of such a collection can be determined based on its physical location.

In order to simultaneously screen for multiple polymorphisms, the nucleic acid markers can be designed for simultaneous use known as multiplexing. Examples of design approaches for multiplexing are set forth in Cho *et al., Nature Genetics 23:*203-207 (1999); Wang *et al., Science 280:* 1077-1082 (1998), the entirety of which is herein incorporated by reference; Winzeler *et al., Curr. Opin. Genet. Dev. 4:* 602-608 (1997), the entirety of which is herein incorporated by reference. Examples of nucleic acid markers that have been optimized for multiplexing are the primers set forth in Table B. Multiplex parameters often require the selection of loci with similar amplification efficiencies, minimizing the concentration of the primers used, and an increased magnesium concentration (Cho *et al., Nature Genetics 23:*203-207 (1999)).

In a preferred embodiment, the polymorphism is present and screened for in a mapping population, *e.g.* a collection of plants capable of being used with markers such as polymorphic markers to map genetic position of traits. The choice of appropriate mapping population often depends on the type of marker systems employed (Tanksley *et al., J.P. Gustafson and R. Appels* (eds.). Plenum Press, New York, pp. 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses

will usually provide segregating populations with a relatively large number of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An F_2 population is the first generation of selfing (self-pollinating) after the hybrid seed is produced. Usually a single F_1 plant is selfed to generate a population segregating for all the genes in Mendelian (1:2:1) pattern. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, Measurement of Linkage in Heredity: Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (*e.g.*, F_3, BCF_2) are required to identify the heterozygotes, in order to classify the population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (*e.g.* disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations *e.g.* F_3 or BCF_2) can be used in map construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2, F_3), where linkage groups have not been completely disassociated by recombination events (*i.e.*, maximum disequilibrium).

Recombinant inbred lines (RIL) (genetically related lines; usually $>F_5$, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (*i.e.*, about <10% recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter. *Proc. Natl. Acad. Sci. (U.S.A.) 89*:1477-1481 (1992), the entirety of which is herein incorporated by reference). However, as the distance between markers becomes larger (*i.e.*, loci become more independent), the information in RIL populations decreases dramatically when compared to codominant markers.

Backcross populations (*e.g.*, generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former) can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al., Proc. Natl. Acad. Sci. (U.S.A.) 89*:1477-1481 (1992), the entirety of which is herein incorporated by reference). Information obtained from backcross populations using either codominant or dominant markers is less than that obtained from F_2 populations because one, rather than two, recombinant gamete is sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (*i.e.* about .15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL) (created by many backcrosses to produce a collection of individuals that is nearly identical in genetic composition except for the trait or genomic region under interrogation) can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci is expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore *et al., Proc. Natl. Acad. Sci. U.S.A. 88*:9828-9832 (1991), the entirety of which is herein incorporated by reference). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but

arbitrary at unlinked regions (*i.e.* heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

While any appropriate mapping population may be used in conjunction with this invention, in a preferred embodiment the mapping population is an *Arabidopsis* population, where the population was created, at least in part, by crossing two different *Arabidopsis* ecotypes, where one of the ecotypes has a phenotype of interest. In an even more preferred embodiment the ecotypes are *Arabidopsis, thaliana,* Columbia and *Arabidopsis, thaliana,* Landsberg *erecta.* In another preferred embodiment, the mapping population is an *Arabidopsis* population, where the population was created, at least in part, by crossing two different *Arabidopsis* ecotypes, where one of the ecotypes has a phenotype of interest, propagating and self pollinating seeds from such a cross and selecting a collection of plants with the phenotype of interest to be the mapping population.

Classical mapping studies often utilize easily observable, visible traits instead of molecular markers. These visible traits are also known as naked eye polymorphisms. These traits can be morphological like plant height, fruit size, shape and color or physiological like disease response, photoperiod sensitivity and crop maturity. Visible traits are useful and are still in use because they represent actual phenotypes and are easy to score without any specialized lab equipment. By contrast, many nucleic acid markers are arbitrary loci for use in linkage mapping and often not associated with specific plant phenotypes (Young, *Encyclopedia of Agricultural Science,* Vol. 3, pp. 275-282 (1994), the entirety of which is herein incorporated by reference). Many morphological markers cause such large effects on phenotype that they are undesirable in breeding programs. Many other visible traits have the disadvantage of being developmentally regulated (*i.e.*, expressed only at certain stages; or in specific tissue and organs). Oftentimes, visible traits mask the effects of linked minor genes making it nearly impossible to identify

desirable linkages for selection (Tanksley *et al., Biotech.* 7:257-264 (1989), the entirety of which is herein incorporated by reference).

Although a number of important agronomic characteristics are controlled by loci having major effects on phenotype, many economically important traits, such as yield and some forms of disease resistance, are quantitative in nature. This type of phenotypic variation in a trait is typically characterized by continuous, normal distribution of phenotypic values in a particular population (polygenic traits) (Beckmann and Soller, *Oxford Surveys of Plant Molecular Biology, Miffen.* (ed.), Vol. 3, Oxford University Press, UK., pp. 196-250 (1986), the entirety of which is herein incorporated by reference). Loci contributing to such genetic variation are often termed minor genes, as opposed to major genes with large effects that follow a Mendelian pattern of inheritance. Polygenic traits are also predicted to follow a Mendelian type of inheritance, however the contribution of each locus is expressed as an increase or decrease in the final trait value. The nucleic acid markers of the present invention can be used to identify and isolate nucleic acid regions or molecules associated with desired polygenic or single gene traits.

In one embodiment, the nucleic acid markers of the present invention are used to isolate or identify an allele of a quantitative trait locus or Mendelian locus.

Nucleic acid markers of the present invention capable of detecting one or more of the polymorphisms may be employed in genetic or physical studies using linkage analysis. Mapping marker genetic locations is based on the observation that two markers located near each other on the same chromosome will tend to be passed together from parent to offspring. During gamete production, DNA strands occasionally break and rejoin in different places on the same chromosome or on the homologous chromosome. The closer the markers are to each other, the more tightly linked and the less likely a recombination event will fall between and separate them. Recombination frequency thus provides an estimate of the distance between two markers.

Linkage analysis is based on the level at which markers and genes are co-inherited (Rothwell, *Understanding Genetics. 4th Ed.* Oxford University Press, New York, p. 703 (1988), the entirety of which is herein incorporated by reference). Statistical tests like chi-square analysis can be used to test the randomness of segregation or linkage (Kochert, *The Rockefeller Foundation International Program on Rice Biotechnology,* University of Georgia Athens, GA, pp. 1-14 (1989), the entirety of which is herein incorporated by reference). In linkage mapping, the proportion of recombinant individuals out of the total mapping population provides the information for determining the genetic distance between the loci (Young, *Encyclopedia of Agricultural Science, Vol. 3*, pp. 275-282 (1994), the entirety of which is herein incorporated by reference). Any statistical analysis that establishes linkage may be used. An example of a suitable linkage approach is Intermap as set forth in Cho *et al., Nature Genetics 23:* 203-207 (1999). Example 6 sets forth another exemplary linkage approach.

In segregating populations, target genes have been reported to have been placed within an interval of 5-10 cM with a high degree of certainty (Tanksley *et al., Trends in Genetics 11(2):*63-68 (1995), the entirety of which is herein incorporated by reference). The markers defining this interval are used to screen a larger segregating population to identify individuals derived from one or more gametes containing a crossover in the given interval. Such individuals are useful in orienting other markers closer to the target gene. Once identified, these individuals can be analyzed in relation to all molecular markers within the region to identify those closest to the target.

Markers of the present invention can be employed to locate genes. The genetic linkage of additional marker molecules can be established by a genetic mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics 121*:185-199 (1989), the entirety of which is herein incorporated by reference, and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics 121*:185-199 (1989), the entirety of which is herein incorporated

by reference and implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL*, Whitehead Institute for Biomedical Research, Massachusetts, (1990), the entirety of which is herein incorporated by reference). Additional software includes Qgene, Version 2.23 (Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY (1996), the manual of which is herein incorporated by reference in its entirety).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of an allele than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, *Genetics 121*:185-199 (1989), the entirety of which is herein incorporated by reference and further described by Arús and Moreno-González, *Plant Breeding*, Hayward, Bosemark, Romagosa (eds.) Chapman & Hall, London, pp. 314-331 (1993), the entirety of which is herein incorporated by reference.

In a preferred embodiment of the present invention the nucleic acid marker exhibits a LOD score of greater than 2.0, more preferably 2.5, even more preferably greater than 3.0 or 4.0 with the trait or phenotype of interest.

Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use of non-parametric methods (Kruglyak and Lander, *Genetics, 139:*1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breed*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding,* Blackwell, Berlin, 16 (1994), the entirety of which is herein incorporated by reference). Procedures combining interval mapping with regression

analysis, whereby the phenotype is regressed onto a single putative QTL at a given interval, and at the same time onto a number of polymorphisms that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics, 136*:1447-1455 (1994), the entirety of which is herein incorporated by reference and Zeng, *Genetics, 136*:1457-1468 (1994), the entirety of which is herein incorporated by reference. Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding,* van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994)), thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics, 136*:1457-1468 (1994), the entirety of which is herein incorporated by reference). These models can be extended to multi-environment experiments to analyze genotype-environment interactions (Jansen *et al., Theo. Appl. Genet. 91:*33-37 (1995), the entirety of which is herein incorporated by reference).

The nucleic acid markers of the present invention may be used to isolate an allele, a region of genomic DNA associated with a phenotype, *etc.* Once the genomic region associated with the phenotype of interest is defined relative to at least one nucleic acid marker, preferably at least two nucleic acid markers capable of detecting different polymorphisms, the genomic region associated with the phenotype may be further characterized. One approach is to select additional nucleic acid markers from the genomic region associated with the trait and localize the genomic region associated with the phenotype to a smaller genomic region by a technique such as fine mapping.

For example, in a preferred embodiment a method for identifying or isolating a genomic region associated with a phenotypic trait that comprises (A) screening a mapping population of *Arabidopsis* plants to determine the linkage of the phenotypic trait with a first collection of polymorphisms, wherein the first collection of polymorphisms is distributed throughout the genome of the mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 500kb - 100kb; (B) calculating

the linkage of each of the first collection of polymorphisms to the phenotypic trait;

(C) identifying a genomic region most closely associated with the phenotypic trait;

(D) selecting a second collection of polymorphisms from the genomic region; and

(E) screening the mapping population of *Arabidopsis* plants to determine the linkage of the phenotypic trait with the second collection of polymorphisms from the genomic region, wherein the second collection of polymorphisms have an average density of more than one polymorphism per about 50kb - 1kb.

In an embodiment of the present invention, for a fine mapping step of the present invention the collection of marker nucleic acids is capable of detecting a characterized polymorphism at a density of greater than one polymorphism per 50kb, more preferably at a density greater than one polymorphism per 25kb, even more preferably at a density greater than one polymorphism per 10kb or 5kb. It is understood, that the fine mapping using such a collection of markers may be carried out, for example, in a single assay or simultaneously.

Once the genomic region associated with the phenotype is identified, the genomic region may be isolated. Alternatively, or in conjunction, such a region may be further defined or characterized. Many approaches are known in the art and may be undertaken (Sambrook *et al.*, *Molecular Cloning 1: A Laboratory Manual*, 2d ed., Ford *et al.*, eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989); Sambrook *et al.*, *Molecular Cloning 2: A Laboratory Manual*, 2d ed., Ford *et al.*, eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989); Sambrook *et al.*, *Molecular Cloning 3: A Laboratory Manual*, 2d ed., Ford *et al.*, eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989); Maliga *et al.*, *Methods in Plant Molecular Biology: A Laboratory Course Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1995); and Birren *et al.*, *Genome Analysis: A Laboratory Manual. Volume 2: Detecting Genes*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1998), all of which are herein incorporated by reference in their entirety).

For example, once identified, the sequence of the genomic region associated with the phenotype may be determined and subjected to bioinformatic analysis (Coulson, *Trends in Biotechnology 12:*76-80 (1994); Birren *et al., Genome Analysis 1,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York 543-559 (1997); Huang, *et al.*, *Genomics 46*:37-45 (1997), all of which are herein incorporated by reference in their entirety). Such bioinformatic approaches can provide, for example, information on the location of putative open reading frames, promoters, and a variety of nucleotide motifs. Moreover, also using bioinformatic approaches, the nucleic acid sequence of the genomic region can be compared with other nucleic acid sequences. Such comparisons can facilitate the isolation of *Arabidopsis* homologs to known genes or genomic regions. Examples of such bioinformation tools are BLAST, GeneScan, GeneMark and AAT.

Other methods can be utilized to further isolate, define, or characterize the genomic region associated with the phenotype. The expression profiles of mRNA and proteins derived from genes that are located within the genetic region associated with the phenotype can be analyzed. Such analysis, will in certain circumstances, allow the gene or genes associated with the phenotype to be determined.

A genomic region or sub-region thereof may be isolated using any of the many techniques in the art. In addition to those procedures and methods set forth herein, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (*e.g.*, DNA molecules, plasmids, *etc.*), generation of recombinant organisms and the screening and isolating of clones, (see, for example, Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989); Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995); Birren *et al., Genome Analysis: Analyzing DNA,* 1, Cold Spring Harbor, New York, all of which are herein incorporated by reference in their entirety).

The biological function of a genomic region or subregion thereof such as a gene or open reading frame, can be further investigated using a mutant complementation approach or other reverse genetics approach. For example, a gene or genes identified within the genomic region associated with the phenotype may be isolated from the organism exhibiting the non-mutant phenotype (often referred to as the wild type). Such a gene or genes may be introduced into an appropriate organism that lacks the phenotype (often referred to as mutant) either by crosses or by molecular genetic techniques such as transformation or transfection. Organisms having the introduced genetic material may be screened to determine whether the introduced gene or genes complements, *i.e.* restores the phenotype of the mutant (Pan, *FEBS Lett. 459(3):* 405-410 (1999); Kerckhoffs *et al., Mol. Gen. Genet. 6:* 901-907 (1999); Lizotte *et al., Gene 234(1):* 35-44 (1999); Berna *et al., Genetics 152:* 729-742 (1999); Liu *et al., Proc. Natl. Acad. Sci. (USA) 96(11):* 6535-6540 (1999); Pia *et al., Plant Physiol. 119(4):* 1527-1534 (1999); Loulergue *et al., Gene 225(1-2):* 47-57 (1998); Jouannic *et al., Eur. J. Bioche,. 258(2):* 402-410 (1998), all of which are herein incorporated by reference in their entirety). While gene or genes *etc.* may be introduced into any organism, preferred organisms are plants, yeasts, and bacteria particularly *E. coli.* In a more preferred embodiment the organism is *Arabidopsis.*

The nucleic acid markers of the present invention may be used for chromosomal walking. Such walking, in conjunction with linkage analysis, can enable the isolation of genes. Once a nucleic acid marker is linked to a region of interest, the chromosome walking technique can be used to find the genes via overlapping clones. For chromosome walking, random molecular markers or established molecular linkage maps are used to conduct a search to localize the gene adjacent to one or more markers capable of detecting a polymorphism. A chromosome walk (Bukanov and Berg, *Mo. Microbiol. 11:*509-523 (1994), the entirety of which is herein incorporated by reference; Birkenbihl and Vielmetter, *Nucleic Acids Res. 17:*5057-5069 (1989), the entirety of which is herein incorporated by reference; Wenzel and Herrmann, *Nucleic Acids Res. 16:*8323-8336,

(1988), the entirety of which is herein incorporated by reference) is then initiated from the closest linked marker. Starting from the selected clones, labeled probes specific for the ends of the insert DNA are synthesized and used as probes in hybridizations against a representative library. Clones hybridizing with one of the probes are picked and serve as templates for the synthesis of new probes; by subsequent analysis, contigs are produced.

The degree of overlap of the hybridizing clones used to produce a contig can be determined by comparative restriction analysis. Comparative restriction analysis can be carried out in different ways all of which exploit the same principle; two clones of a library are very likely to overlap if they contain a limited number of restriction sites for one or more restriction endonucleases located at the same distance from each other. The most frequently used procedures are, fingerprinting (Coulson *et al., Proc. Natl. Acad. Sci. (U.S.A.) 83*:7821-7821, (1986), the entirety of which is herein incorporated by reference; Knott *et al., Nucleic Acids Res. 16*:2601-2612 (1988), the entirety of which is herein incorporated by reference; Eiglmeier *et al. Mol. Microbiol.* 7:197-206 (1993), the entirety of which is herein incorporated by reference), restriction fragment mapping (Smith and Birnstiel, *Nucleic Acids Res.* 3:2387-2398 (1976), the entirety of which is herein incorporated by reference), and the "landmarking" technique (Charlebois *et al. J. Mol. Biol.* 222:509-524 (1991), the entirety of which is herein incorporated by reference).

It is understood that the nucleic acid molecules of the present invention may in one embodiment be used for chromosomal walking. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used in the chromosomal walking of *Brassicaceae,* particularly *Arabidopsis.*

Nucleic acid markers of the present invention can be used in comparative mapping and comparative chromosomal walking. Comparative mapping within families provides a method to assess the degree of sequence conservation, gene order, ploidy of species, ancestral relationships and the rates at which individual genomes are evolving. It also provides a method to isolate genetic regions or sub-aspects thereof such as genes.

Comparative mapping has been carried out by utilizing molecular markers from one species with another species. As in genetic mapping, nucleic acid markers are needed but instead of direct hybridization to mapping filters, the markers can also be used to select large insert clones from a total genomic DNA library of a related species. The selected clones can then be used to physically map the region in the target species. The advantage of this method for comparative mapping is that no mapping population or linkage map of the target species is needed and the clones may also be used in other closely related species. By comparing the results obtained by genetic mapping in model plants, with those from other species, similarities of genomic structure among plants species can be established. Comparative mapping using nucleic acid markers of the present invention permits the identification and/or isolation of non-*Arabidopsis* syntenic regions and homolog genes with such regions.

It is understood that nucleic acid markers of the present invention may in another embodiment be used in comparative mapping. In a preferred embodiment the markers of the present invention may be used in the comparative mapping of non-*Arabidopsis* plant species, including but not limited to alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, maize, pea, peanut, pepper, potato, rice, rye, sorghum, soybean, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, *Phaseolus etc.* Particularly preferred non-*Arabidopsis* plants to utilize for comparative mapping are the *Brassicaceae*.

Agents of the present invention include nucleic acid molecules and more specifically include nucleic acid markers capable of detecting polymorphisms. In a preferred embodiment the nucleic acid molecules of the present invention are derived from *Arabidopsis* and in an even more preferred embodiment the nucleic acid molecules of the present invention are derived from *Arabidopsis thaliana,* Landsberg *erecta* or *Arabidopsis thaliana,* Columbia.

In another preferred embodiment, the nucleic acid molecules of the present invention include those isolated utilizing the nucleic acid markers of the present invention. The present invention also encompasses the use of these and other nucleic acids of the present invention in recombinant constructs. Using methods known to those of ordinary skill in the art, such molecules can be introduced into a host cell or organism of choice. Potential host cells include both prokaryotic and eukaryotic cells. A host cell may be unicellular or found in a multicellular differentiated or undifferentiated organism depending upon the intended use. It is understood that useful exogenous genetic material may be introduced into any cell or organism such as a plant cell, plant, mammalian cell, mammal, fish cell, fish, bird cell, bird or bacterial cell.

In a preferred embodiment the exogenous DNA is introduced into a plant in a suitable construct. Preferred plants are selected from the group consisting of: alfalfa, *Arabidopsis,* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, soybean, and *Phaseolus*. A particularly preferred group of plants is rice, cotton, wheat, maize and soybean.

As used herein, an agent, be it a naturally occurring molecule or otherwise may be "substantially purified," if, referring to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to

another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

The agents of the present invention may can also be recombinant. As used herein, the term recombinant describes (a) nucleic acid molecules that are constructed or modified outside of cells and that can replicate or function in a living cell, (b) molecules that result from the transcription, replication or translation of recombinant nucleic acid molecules , or (c) organisms that contain recombinant nucleic acid molecules or are modified using recombinant nucleic acid molecules.

It is understood that the agents of the present invention may be labeled with reagents that facilitate detection of the agent (*e.g.* fluorescent labels, Prober *et al., Science* *238*:336-340 (1987); Albarella *et al.,* EP 144914, chemical labels, Sheldon *et al.,* U.S. Patent 4,582,789; Albarella *et al.,* U.S. Patent 4,563,417, modified bases, Miyoshi *et al.,* EP 119448, all of which are herein incorporated by reference in their entirety).

Fragment nucleic acid molecules may encode significant portion(s) of, or indeed most of, these nucleic acid molecules. For example, a fragment nucleic acid molecule can encode an *Arabidopsis* protein or fragment thereof. Alternatively, the fragments may comprise smaller oligonucleotides. Exemplary fragment sizes include fragments having from about 15 to about 400 nucleotide residues and more preferably, about 15 to about 30 nucleotide residues, or about 50 to about 100 nucleotide residues, or about 100 to about 200 nucleotide residues, or about 200 to about 400 nucleotide residues, or about 275 to about 350 nucleotide residues.

Nucleic acid molecules or fragments thereof of the present invention are capable of specifically hybridizing to other nucleic acid molecules under certain circumstances. As used herein, two nucleic acid molecules are said to be capable of specifically hybridizing to one another if the two molecules are capable of forming an anti-parallel,

double-stranded nucleic acid structure. A nucleic acid molecule is said to be the "complement" of another nucleic acid molecule if they exhibit complete complementarity. As used herein, molecules are said to exhibit "complete complementarity" when every nucleotide of one of the molecules is complementary to a nucleotide of the other. Two molecules are said to be "minimally complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under at least conventional "low-stringency" conditions. Similarly, the molecules are said to be "complementary" if they can hybridize to one another with sufficient stability to permit them to remain annealed to one another under conventional "high-stringency" conditions. Conventional stringency conditions are described by Sambrook *et al.*, *Molecular Cloning,* A Laboratory Manual, 2nd Ed., Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), and by Haymes *et al. Nucleic Acid Hybridization, A Practical Approach*, IRL Press, Washington, DC (1985), the entirety of which is herein incorporated by reference. Departures from complete complementarity are therefore permissible, as long as such departures do not completely preclude the capacity of the molecules to form a double-stranded structure. Thus, in order for a nucleic acid molecule to serve as a primer or probe it need only be sufficiently complementary in sequence to be able to form a stable double-stranded structure under the particular solvent and salt concentrations employed.

Appropriate stringency conditions which promote DNA hybridization, for example, 6.0 X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0 X SSC at 50°C, are known to those skilled in the art or can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6, the entirety of which is herein incorporated by reference. For example, the salt concentration in the wash step can be selected from a low stringency of about 2.0 X SSC at 50°C to a high stringency of about 0.2 X SSC at 50°C. In addition, the temperature in the wash step can be increased from low stringency conditions at room temperature, about 22°C, to high

stringency conditions at about 65°C. Both temperature and salt may be varied, or either the temperature or the salt concentration may be held constant while the other variable is changed.

Hybridizations involving at least one oligonucleotide can necessitate changes from the above hybridization conditions. Highly stringent conditions are often selected to be equal to the T_m point for a particular probe. Sometimes the term "T_d" is used to define the temperature at which at least half of the probe dissociates from a perfectly matched target nucleic acid. In any case, a variety of estimation techniques for estimating the T_m or T_d are available, and generally described in Tijssen, *id.* Typically, G-C base pairs in a duplex are estimated to contribute about 3°C to the T_m, while A-T base pairs are estimated to contribute about 2°C, up to a theoretical maximum of about 80-100°C. However, more sophisticated models of T_M and T_d are available and appropriate in which G-C stacking interactions, solvent effects, the desired assay temperature and the like are taken into account. For example, PCR primers can be designed to have a dissociation temperature (T_d) of approximately 60°C, using the formula: T_d = (((((3 x #GC) + (2 x #AT)) x 37) - 562) / #bp) - 5; where #GC, #AT, and #bp are the number of guanine-cytosine base pairs, the number of adenine-thymine base pairs, and the number of total base pairs, respectively, involved in the annealing of the primer to the template DNA.

Nucleic acid markers of the present invention can be used to characterize transformants or germplasm, as a genetic diagnostic test for plant breeding or to identify individuals or varieties (Soller and Beckmann, *Theor. Appl. Genet.* (67):25-33 (1983), the entirety of which is herein incorporated by reference). Such markers can also be used to obtain information about: (1) the number, effect, and chromosomal location of each gene affecting a trait; (2) effects of multiple copies of individual genes (gene dosage); (3) interaction between/among genes controlling a trait (epistasis); (4) whether individual genes affect more than one trait (pleiotropy); and (5) stability of gene function across environments (Gx E interactions).

In a preferred embodiment, the nucleic acid markers of the present invention may be used in marker assisted introgression of traits into plants. Marker assisted introgression involves the transfer of a chromosome region defined by one or more markers from one germplasm to a second germplasm. An initial step in such a process is the localization of the trait or region by mapping. One use of marker assisted introgression of genomic regions is in the generation of near isogenic lines (NILs) or recombinant near isogenic lines (RILs). In one aspect of the present invention, the nucleic acid markers are used to generate *Arabidopsis* NILs or RILs. As used herein, introgression is the process of transferring a genetic region from one genetic background to a second but non-identical genetic background.

Additional markers, such as AFLP markers, RFLP markers, RAPD markers, SNPs, phenotypic markers, isozyme markers can be utilized in combination with or separately from the markers of the invention (Walton, Seed World 22-29 (1993), the entirety of which is herein incorporated by reference; Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Eds. Paterson, CRC Press, New York (1988), the entirety of which is herein incorporated by reference). Examples of additional markers are set forth in Cho *et al., Nature Genetics 23:* 203-205 (1999).

DNA markers can be developed from nucleic acid molecules using restriction endonucleases, the PCR and/or DNA sequence information. RFLP can result from single base changes or insertions/deletions. RFLP are highly abundant in plant genomes, have a medium level of polymorphism and are developed by a combination of restriction endonuclease digestion and Southern blotting hybridization. CAPS are similarly developed from restriction nuclease digestion but only of specific PCR products. CAPS are also codominant, have a medium level of polymorphism and are highly abundant in the genome. The CAPS result from single base changes and insertions/deletions. RAPDs are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. RAPDs with a medium level of

polymorphisms are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. AFLPs are both dominant and codominant are highly abundant in genomes and exhibit a medium level of polymorphism. SSRs require DNA sequence information. SSRs result from repeat length changes, are highly polymorphic, and do not exhibit as high a degree of abundance in the genome as CAPS, AFLPs and RAPDs. SNPs also require DNA sequence information. SNPs result from single base substitutions. They are highly abundant and exhibit a medium of polymorphism (Rafalski *et al.*, In: *Nonmammalian Genomic Analysis*, ed. Birren and Lai, Academic Press, San Diego, CA, pp. 75-134 (1996), the entirety of which is herein incorporated by reference).

Computer Readable Media

A polymorphism or nucleic acid molecule of the present invention can be "provided" in a variety of mediums to facilitate use. Moreover, the nucleic acid markers and other nucleic acid molecules of the present invention may also be so presented.

In one embodiment, a polymorphism may be presented in a manner that sets forth 1, more preferably 2, 3, 4, 5, 6, or 7 of the following features alone or in combination with other features: (1) type of polymorphism (*e.g.* SNP, insertion, deletion *etc.*); (2) physical location of the polymorphism on a chromosome; (3) nucleotide sequence variation associated with one or more of the alleles; (4) nucleotide sequences of nucleic acid marker molecules capable of detecting the polymorphism; (5) physical location of the polymorphism relative to a piece of isolated DNA (*e.g.*, BAC); (6) methodology for detecting the polymorphism; (7) physical distance from that polymorphism to another polymorphism; and (8) genetic linkage with a phenotype or other polymorphism.

Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine these features.

In one application of this embodiment, a polymorphism and associated features of the present invention can be recorded on computer readable media. In another embodiment, a nucleic acid sequence of the present invention can be recorded on computer readable media alone or in combination with a polymorphisms and associated features. As used herein, "computer readable media" refers to any medium that can be read or accessed by a computer, either directly or indirectly through a network. Such media include, but are not limited to: magnetic storage media, such as disks or magnetic tape; optical storage media such as optical disks; electrical storage media such as read-only memory (ROM) or Random Access Memory (RAM); and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the known methods for recording information on computer readable medium to generate media comprising the information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of application programs and formats can be used to store the information of the present invention on computer readable medium. The sequence information can be represented, for example, in a word processing file, formatted in commercially-available software such as WordPerfect and Microsoft Word, in a network-accessible format, such as an HTML file or web page, an ASCII file, or stored in a database application, such as DB2, Excel, Sybase, Oracle, or the like. A skilled artisan can readily adapt any number of data file formats (*e.g.*, text file or database) or data

structures in order to obtain computer readable medium having recorded thereon the information of the present invention.

A skilled artisan is provided with access to the information for a variety of purposes. Publicly available computer software allows a skilled artisan to access, for example, sequence information provided in a computer readable medium.

The present invention further provides systems, particularly computer-based systems, which contain the information described herein. As used herein, "a computer-based system" refers to the hardware, software, and data storage used to analyze the information including the nucleic acid sequence information of the present invention. The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input/output apparatus, and data storage. A skilled artisan can readily appreciate that any one of the currently available computer-based systems are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage having stored therein a polymorphism and any associated information of the present invention and the necessary hardware and software for supporting and implementing a search. As used herein, "data storage" refers to memory that can store information of the present invention, or a memory access apparatus (hardware and/or software) that can access manufactures having recorded thereon the information of the present invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

Assembled *Arabidopsis thaliana,* Landsberg *erecta* nucleic acid sequence is generated essentially as set forth below:

DNA Preparation

DNA from *Arabidopsis thaliana,* Landsberg *erecta* seedlings is prepared by a CTAB genomic DNA isolation protocol as described by Dean *et al. Plant J* 2:69-81(1992) and modified by Dubois *et al. Plant J. 13*:141-151 (1998), the entirety of which is herein incorporated by reference.

A solution of DNA to be sheared is prepared in a 1.5 ml microcentrifuge tube by mixing 15 μg of DNA, 6 μl of 10X mung bean (MB) buffer (10X MB buffer = 300mM NaOAc, pH 5.0, 500 mM NaCl, 10 mM $ZnCl_2$, 50% glycerol), and water to a final volume of 60 μl. The DNA solution is kept on ice prior to sonication. For sonication, a cup horn probe chilled with ice water for 1 hour prior to sonication is used. The sonicator (Ultrasonic Liquid Processor XL2020 , Misonix Inc.) is pulsed for approximately 10 seconds on full power prior to use. DNA samples are sonicated twice for 6 seconds each at 60% power. Four sample tubes may be processed at once in a multi-tube rack which is positioned 1 to 3 mm above the opening in the probe. The DNA is returned to ice and a 1 μl sample is analyzed by electrophoresis on a 0.8% agarose gel in 0.5X TBE gel, run at 60 volts for 30 minutes. Sonication may be repeated if necessary.

A 0.26 μl aliquot of mung bean nuclease (150,000 u/ml) is added to sheared DNA and the sample is incubated at 30° C for 10 minutes. To stop the digestion, 20 μl of 1 M NaCl, 140 μl dd H_20, and 200 ml of phenol:chloroform are added to the sample which is then vortexed and centrifuged for 20 minutes at 13,000 rpm. The resulting aqueous phase is transferred into a new 1.5 ml microcentrifuge tube, 500 μl of 95% ethanol is added, and the DNA is precipitated overnight at -80° C. The sample is centrifuged for 30 minutes at 13,000 rpm, washed with 500 μl of 95% ethanol and centrifuged again for 30 minutes at 13,000rpm. The sample is then dried under vacuum, and resuspended in 10 μl TE.

The sheared DNA fragments are sized and purified by preparative agarose gel electrophoresis. Five microliters of 6x BP-XC-glycerol dye (0.25% BP, 0.25% XC, 30% glycerol) is added to the sample. The sample is split into two samples and loaded (12.5

µl per lane) on a 0.8% (1x TAE) low-melting agarose gel (SeaPlaque GTG) and electrophoresed at 60 V, 46 mA for 3.5 hours.

The gel is photographed under long wave UV and slices containing DNA fragments of 1.3 - 1.7 kb and 2 - 4 kb are excised and excess agarose cut away. The gel slices are placed in 1.5 ml microcentrifuge tubes. One gel slice is stored at -20° C. 15 µl of 1 M NaCl is added to the other gel slice, followed by melting of the agarose by incubation at 65° C for 8 minutes. The resulting approximately 250 µl samples are placed into microcentrifuge tubes. An equal volume of water is added, following which the sample is vortexed and placed at room temperature for 2 minutes to bring the temperature up to 30 -35° C. 0.5 ml of water-saturated phenol that has been cooled on ice is added and the sample vortexed vigorously. The sample is placed on ice for 5 minutes, and the vortexing step repeated.

The sample is centrifuged at 4°C in a microcentrifuge for 20 minutes. The upper phase is transferred to a clean tube, and the bottom phenol layer is reextracted by addition of 200 µl of dd H_2O. The sample is vortexed and placed on ice for 5 minutes, followed by centrifugation for 15 minutes. The aqueous layer is extracted and added to the aqueous layer from the previous step. Phenol extraction is repeated with 0.5 ml phenol, followed by vortexing and centrifugation for 20 minutes at 4°C. The aqueous layer is removed and repeated sec-butanol extractions are performed until the final volume is reduced to approximately 0.165 ml.

Two volumes of 95% ethanol (400 µl) are added and the sample is stored at -80° C overnight. The sample is centrifuged for 30 minutes at room temperature to pellet the DNA, washed once with 95% ethanol and dried briefly under vacuum. The sample is resuspended in 7 µl of TE. A 1 µl sample is run on a 0.8% agarose gel with markers to estimate concentration of recovered fraction.

M13 Library

20 ng of M13 DNA digested with *Sma*I is mixed with 1 µl of 10x ligation buffer (10X ligation buffer = 0.5M tris pH 7.4, 0.1M $MgCl_2$, 0.1M DDT), 1µl of 1mM ATP and 100 - 200 ng of sheared genomic DNA fragments (1 - 3 µl volume), and 0.3 µl of high concentration NEB ligase (5 unit/µl) is added. Water is added to a final volume of 10µl and the sample is incubated overnight at 14° C.

Plasmid Library

200 ng (4 µl) of pSTBlue vector (Novegene) is mixed with approximately 600 ng (12 µl) of sheared genomic DNA fragments from the 2-4kb size range gel slices and 1.2 µl of Gibco T4 ligase (5 units per µl) is added. Water is added to a final volume of 30µl and the sample is incubated overnight at 14° C.

Transformation

The ligation reaction is titered and diluted for optimal transformation efficiency. When the ligation contains approximately 20 ng of M13 vector, the dilution will typically be from 1:25 to 1:100. A 1:25 dilution is used for plasmid ligation containing approximately 200 ng of vector DNA. To increase transformation efficiency, the ligase is denatured by heating at 65°C for 7 minutes, and placed at room temperature for 5 minutes following the heating step.

A sterile electroporation cuvette is chilled for each transformation. Electro-competent cells are removed from the -80° C freezer and thawed on ice. For each M13 transformation, a sterile tube containing 25 ul of IPTG (25 mg/ml in water), 25 µl of X-Gal (25 mg/ml in dimethylformamide) and 3 ml of YT top agar is prepared, capped and placed in a 45° C water bath. YT plates are pre-warmed at 37° C for several hours to avoid cross-contamination problems that may result if water remains on plates. For plasmid transformations, a sterile tube containing 0.5 ml of SOC medium is prepared for each transformation, and L + amp plates are pre-spread with 25 µl of IPTG and 25 µl of X-Gal.

25 µl of electro-competent cells are mixed with DNA in diluted ligation mix in the cuvette, and the sample pulsed in an *E. coli* pulser (BioRad) set to the appropriate voltage (1.80kV for 0.1 cm cuvettes; 2.50kV for 0.2 cm cuvettes). The cuvette is removed from the pulser, and the sample immediately transferred to the tube containing SOC or YT top agar. For M13 transfections, the sample is plated immediately on YT plates. For plasmid transformations, the tube is placed in a 37° C shaker for 15-30 minutes and 30 ul aliquots are plated on L + Amp plates. Plates are incubated at 37° C overnight.

Two basic methods can be used for DNA sequencing, the chain termination method of Sanger *et al., Proc. Natl. Acad. Sci. (U.S.A.) 74:*5463-5467 (1977), the entirety of which is herein incorporated by reference and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci. (U.S.A.) 74:*560-564 (1977), the entirety of which is herein incorporated by reference. Automation and advances in technology such as the replacement of radioisotopes with fluorescence-based sequencing have reduced the effort required to sequence DNA (Craxton, *Methods 2:*20-26 (1991), the entirety of which is herein incorporated by reference; Ju *et al., Proc. Natl. Acad. Sci. (U.S.A.) 92:*4347-4351 (1995), the entirety of which is herein incorporated by reference; Tabor and Richardson, *Proc. Natl. Acad. Sci. (U.S.A.) 92:*6339-6343 (1995), the entirety of which is herein incorporated by reference). Automated sequencers are available from, for example, Pharmacia Biotech, Inc., Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000) and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required to sequence DNA and such advances provide a rapid high resolution approach for sequencing DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res.. 18*:1415-1419 (1990); Smith, *Nature 349*:812-813 (1991); Luckey *et al.*, *Methods Enzymol. 218*:154-172 (1993); Lu *et al.*, *J. Chromatog. A. 680*:497-501 (1994); Carson *et al.*, *Anal.*

Chem. 65:3219-3226 (1993); Huang *et al.*, *Anal. Chem. 64*:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis 17*:1852-1859 (1996); Quesada and Zhang, *Electrophoresis 17*:1841-1851 (1996); Baba, *Yakugaku Zasshi 117*:265-281 (1997), all of which are herein incorporated by reference in their entirety).

A number of sequencing techniques are known in the art, including fluorescence-based sequencing methodologies. These methods have the detection, automation and instrumentation capability necessary for the analysis of large volumes of sequence data. Currently, the 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allows the most rapid electrophoresis and data collection. With these types of automated systems, fluorescent dye-labeled sequence reaction products are detected and data entered directly into the computer, producing a chromatogram that is subsequently viewed, stored, and analyzed using the corresponding software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al., Genome Analysis: Analyzing DNA*,1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

PHRED is used to call the bases from the sequence trace files (http://www.mbt.washington.edu). PHRED uses Fourier methods to examine the four base traces in the region surrounding each point in the data set in order to predict a series of evenly spaced predicted locations. That is, it determines where the peaks would be centered if there are no compressions, dropouts, or other factors shifting the peaks from their "true" locations. Next, PHRED examines each trace to find the centers of the actual, or observed peaks and the areas of these peaks relative to their neighbors. The peaks are detected independently along each of the four traces so many peaks overlap. A dynamic programming algorithm is used to match the observed peaks detected in the second step with the predicted peak locations found in the first step.

After the base calling is completed, two sequence quality steps occur 1) poor quality end sequences are cut and if the resulting sequence is 50 bp or less it is deleted 2) overall sequence quality is examined and poor sequences are deleted from the data set if

they have an average quality cutoff below 12.5. Contaminating sequences (*E. coli*, yeast, vector, linker) are removed after sequence quality assessment.

Contigs are assembled using PANGEA clustering tools (PANGEA SYSTEMS. INC) and PHRAP (http://www.mbt.washington.edu). PANGEA clustering tools are a series of scripts which group sequences (clusters) by comparing pairs of sequences for overlapping bases. The overlap is determined using the following high stringency parameters: word size = 8; window size = 60; and identity is 93%. Each of the clusters are then assembled using PHRAP. The final assembly output contains a collection of sequences including contigs, sequences representing the consensus sequence of overlapping clustered sequences, and singletons, sequences which are not present in any cluster of related sequences. Collectively, the contigs and singletons resulting from a DNA assembly are referred to as islands.

Example 2

INDELs are identified by aligning sequences from *Arabidopsis thaliana,* Columbia and *Arabidopsis thaliana,* Landsberg *erecta.* Finished BAC sequences derived from *Arabidopsis thaliana,* Columbia are obtained from GenBank (http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=Nucleotide). Because the GenBank sequences are subject to change, the finished sequences of the *Arabidopsis thaliana,* Columbia BACs are included herein as SEQ ID NO: 1 through SEQ ID NO: 124. The sequence of each *Arabidopsis thaliana,* Columbia BAC is used as a query against a database of *Arabidopsis thaliana,* Landsberg *erecta* islands using the GAP2 program of the Analysis and Annotation Tool (AAT) for Finding Genes in Genomic Sequences which was developed by Xiaoqiu Huang at Michigan Tech University and is available at the web site http://genome.cs.mtu.edu/. See Huang, *et al., Genomics 46*: 37-45 (1997) and Huang, *Computer Applications in the Biosciences 10* 227-235 (1994), both of which are herein incorporated by reference in their entirety. The GAP2 program compares the query sequence with a cDNA database using a fast database search program and a rigorous alignment program. The database search program quickly identifies regions of the query sequence that are similar to a database sequence. Then the alignment program

constructs an optimal alignment for each region and the database sequence. The output file of GAP2 is reviewed for insertions or deletions. Using alignments that are at least 96% identical (as reported by AAT), insertions and deletions are determined by looking for gaps of at least three bases, with three aligned bases on either side of the gap. To ensure that an insertion or deletion is derived from matched sequence, the 10bp region to either side of the gap is aligned and compared. To be considered an insertion or deletion, the adjacent aligned regions must be at least 90% identical (as reported by AAT). Insertions or deletions smaller than 100bp are considered candidate markers. INDELs identified by the method of this Example 2 are set forth in Table A and identified in the "method" column by reference to method 2. More particularly Table A identifies the location and nature of the polymorphism as follows:

"Seq Num" refers to the sequence of the finished BAC of *Arabidopsis thaliana,* ecotype Columbia where the polymorphism can be found;

"Seq id" refers to an arbitrary name used by applicant to identify the BAC sequence;

"Chromosome" refers to the chromosome of *Arabidopsis thaliana* in which the polymorphism is located;

"BAC Length" refers to the number of nucleotides in the finished BAC sequence;

"BAC Name" refers to the name of the BAC as used in GenBank;

"Marker Name" refers to a unique six digit number arbitrarily set by applicant for a polymorphism;

"Left" refers to the position of the closest nucleotide in the flanking sequence on the 5' side of the polymorphism;

"Right" refers to the position of the closest nucleotide in the flanking sequence on the 3' side of the polymorphism;

"Type" refers to identification of the polymorphism as a SNP or IND (*i.e.*, INDEL);

"Method" refers to the method used to identify the polymorphism, where "1" represents the method of Example 3 used to detect SNPs and INDELs of less than 3

nucleotides and "2" represents the method of Example 2 used to detect large INDELs; and

"Indel Size Columbia/Landsberg" refers to the size of INDELs in terms of "n/-n" or "-n/n", where n is the size of the insertion or deletion and the minus sign indicates the ecotype with the smaller sequence length in the area of the polymorphism.

SNP Base Columbia/Landsberg" describes the nucleotide base of a SNP in the respective ecotypes, *e.g.* "T/C."

Table A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
1	AC009273	1	76175	T1N6	468405	61032	61034	SNP	1		G/A
1	AC009273	1	76175	T1N6	468406	62183	62185	SNP	1		C/A
1	AC009273	1	76175	T1N6	468407	59723	59725	SNP	1		G/A
1	AC009273	1	76175	T1N6	468408	62310	62312	SNP	1		T/C
1	AC009273	1	76175	T1N6	468409	61729	61731	SNP	1		A/C
1	AC009273	1	76175	T1N6	468410	62311	62313	SNP	1		A/T
1	AC009273	1	76175	T1N6	468575	66144	66146	SNP	1		T/C
1	AC009273	1	76175	T1N6	468576	64563	64565	SNP	1		A/T
1	AC009273	1	76175	T1N6	470714	41645	41748	IND	2	102/-102	
1	AC009273	1	76175	T1N6	470715	42837	42838	IND	2	-3/3	
1	AC009273	1	76175	T1N6	470716	49675	49676	IND	2	-6/6	
1	AC009273	1	76175	T1N6	470717	53840	53841	IND	2	-4/4	
1	AC009273	1	76175	T1N6	471481	39536	39537	IND	1	-1/1	
1	AC009273	1	76175	T1N6	471482	59752	59754	IND	1	1/-1	
1	AC009273	1	76175	T1N6	471483	69644	69645	IND	1	-1/1	
2	AC020622	1	45013	F22M8	469132	1662	1664	SNP	1		G/T
2	AC020622	1	45013	F22M8	469136	9637	9639	SNP	1		T/A
3	AC007583	1	107234	F24B9	469902	16214	16225	IND	2	10/-10	
3	AC007583	1	107234	F24B9	469903	18885	18886	IND	2	-4/4	
3	AC007583	1	107234	F24B9	469904	24350	24351	IND	2	-57/57	
3	AC007583	1	107234	F24B9	469905	32257	32258	IND	2	-14/14	
3	AC007583	1	107234	F24B9	469906	32257	35375	IND	2	3117/-3117	
3	AC007583	1	107234	F24B9	469907	38282	38291	IND	2	8/-8	
3	AC007583	1	107234	F24B9	469908	4445	4446	IND	2	-15/15	
3	AC007583	1	107234	F24B9	469909	51271	51275	IND	2	3/-3	
3	AC007583	1	107234	F24B9	469910	67592	67599	IND	2	6/-6	
3	AC007583	1	107234	F24B9	469911	69736	69737	IND	2	-12/12	
3	AC007583	1	107234	F24B9	469912	70790	70795	IND	2	4/-4	
3	AC007583	1	107234	F24B9	469913	75121	75122	IND	2	-12/12	
3	AC007583	1	107234	F24B9	469914	75123	75124	IND	2	-12/12	
3	AC007583	1	107234	F24B9	469915	76325	76333	IND	2	7/-7	
3	AC007583	1	107234	F24B9	469916	76364	76373	IND	2	8/-8	
3	AC007583	1	107234	F24B9	469917	76398	76405	IND	2	6/-6	
3	AC007583	1	107234	F24B9	469918	85617	85624	IND	2	6/-6	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
3	AC007583	1	107234	F24B9	469919	86485	86491	IND	2	5/-5	
3	AC007583	1	107234	F24B9	469920	96586	96587	IND	2	-4/4	
3	AC007583	1	107234	F24B9	469921	98779	98780	IND	2	-3/3	
4	AC012187	1	74328	F13K23	472002	26800	26802	SNP	1		C/A
4	AC012187	1	74328	F13K23	472003	26917	26919	SNP	1		C/A
4	AC012187	1	74328	F13K23	472004	27391	27393	SNP	1		A/G
4	AC012187	1	74328	F13K23	472005	26751	26753	SNP	1		C/T
4	AC012187	1	74328	F13K23	472241	48517	48519	SNP	1		T/A
4	AC012187	1	74328	F13K23	472242	48649	48651	SNP	1		C/T
4	AC012187	1	74328	F13K23	472372	12021	12023	SNP	1		G/A
4	AC012187	1	74328	F13K23	472373	12523	12525	SNP	1		G/C
4	AC012187	1	74328	F13K23	472687	45187	45189	SNP	1		T/G
4	AC012187	1	74328	F13K23	472745	65810	65812	SNP	1		G/C
4	AC012187	1	74328	F13K23	472746	65765	65767	SNP	1		A/G
4	AC012187	1	74328	F13K23	472936	67896	67898	SNP	1		C/A
4	AC012187	1	74328	F13K23	472937	68221	68223	SNP	1		A/T
4	AC012187	1	74328	F13K23	472938	67895	67897	SNP	1		C/T
4	AC012187	1	74328	F13K23	473013	24350	24352	SNP	1		T/A
4	AC012187	1	74328	F13K23	473037	64000	64002	SNP	1		T/G
4	AC012187	1	74328	F13K23	473163	42906	42908	SNP	1		A/G
4	AC012187	1	74328	F13K23	473433	14866	14868	SNP	1		T/A
4	AC012187	1	74328	F13K23	473434	15600	15602	SNP	1		G/A
4	AC012187	1	74328	F13K23	473435	15552	15554	SNP	1		T/G
4	AC012187	1	74328	F13K23	473579	727	729	SNP	1		T/C
4	AC012187	1	74328	F13K23	473580	793	795	SNP	1		C/T
4	AC012187	1	74328	F13K23	473581	108	110	SNP	1		C/T
4	AC012187	1	74328	F13K23	473620	47143	47145	SNP	1		G/A
4	AC012187	1	74328	F13K23	473621	46952	46954	SNP	1		G/A
4	AC012187	1	74328	F13K23	473622	46887	46889	SNP	1		T/A
4	AC012187	1	74328	F13K23	473623	46886	46888	SNP	1		T/A
4	AC012187	1	74328	F13K23	473624	47021	47023	SNP	1		A/T
4	AC012187	1	74328	F13K23	473625	46889	46891	SNP	1		C/T
4	AC012187	1	74328	F13K23	473821	21544	21545	IND	2	-6/6	
4	AC012187	1	74328	F13K23	473822	28358	28359	IND	2	-3/3	
4	AC012187	1	74328	F13K23	473823	28825	28826	IND	2	-54/54	
4	AC012187	1	74328	F13K23	473824	30476	30481	IND	2	4/-4	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
4	AC012187	1	74328	F13K23	473825	31803	31807	IND	2	3/-3	
4	AC012187	1	74328	F13K23	473826	31859	31872	IND	2	12/-12	
4	AC012187	1	74328	F13K23	473827	349	350	IND	2	-3/3	
4	AC012187	1	74328	F13K23	474047	14241	14242	IND	1	-2/2	
4	AC012187	1	74328	F13K23	474048	24020	24021	IND	1	-1/1	
4	AC012187	1	74328	F13K23	474049	354	355	IND	1	-2/2	
4	AC012187	1	74328	F13K23	474050	43082	43083	IND	1	-1/1	
4	AC012187	1	74328	F13K23	474051	46892	46896	IND	1	3/-3	
4	AC012187	1	74328	F13K23	474052	73893	73894	IND	1	-1/1	
5	AC012188	1	111686	F14L17	467114	8011	8013	SNP	1		A/C
5	AC012188	1	111686	F14L17	467115	8140	8142	SNP	1		T/C
5	AC012188	1	111686	F14L17	467116	8010	8012	SNP	1		G/T
5	AC012188	1	111686	F14L17	467979	38075	38077	SNP	1		A/T
5	AC012188	1	111686	F14L17	467980	39802	39804	SNP	1		A/T
5	AC012188	1	111686	F14L17	468122	5897	5899	SNP	1		T/C
5	AC012188	1	111686	F14L17	468123	68782	68784	SNP	1		G/A
5	AC012188	1	111686	F14L17	468637	84816	84818	SNP	1		A/T
5	AC012188	1	111686	F14L17	468638	85085	85087	SNP	1		A/T
5	AC012188	1	111686	F14L17	468662	50657	50659	SNP	1		T/G
5	AC012188	1	111686	F14L17	468726	80329	80331	SNP	1		A/G
5	AC012188	1	111686	F14L17	468752	12165	12167	SNP	1		C/A
5	AC012188	1	111686	F14L17	468753	12012	12014	SNP	1		T/C
5	AC012188	1	111686	F14L17	468754	12589	12591	SNP	1		A/G
5	AC012188	1	111686	F14L17	468755	16372	16374	SNP	1		T/A
5	AC012188	1	111686	F14L17	468756	16761	16763	SNP	1		G/A
5	AC012188	1	111686	F14L17	468757	17420	17422	SNP	1		T/A
5	AC012188	1	111686	F14L17	468758	14585	14587	SNP	1		T/C
5	AC012188	1	111686	F14L17	468759	15162	15164	SNP	1		T/C
5	AC012188	1	111686	F14L17	468760	16364	16366	SNP	1		A/C
5	AC012188	1	111686	F14L17	468761	13252	13254	SNP	1		T/C
5	AC012188	1	111686	F14L17	468762	13345	13347	SNP	1		A/G
5	AC012188	1	111686	F14L17	468763	14314	14316	SNP	1		G/T
5	AC012188	1	111686	F14L17	468764	15638	15640	SNP	1		A/T
5	AC012188	1	111686	F14L17	468765	13213	13215	SNP	1		G/T
5	AC012188	1	111686	F14L17	468766	16184	16186	SNP	1		C/T
5	AC012188	1	111686	F14L17	468883	56851	56853	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
5	AC012188	1	111686	F14L17	468970	10113	10115	SNP	1		G/C
5	AC012188	1	111686	F14L17	469164	44311	44313	SNP	1		A/G
5	AC012188	1	111686	F14L17	469165	44327	44329	SNP	1		A/T
5	AC012188	1	111686	F14L17	469228	28002	28004	SNP	1		T/C
5	AC012188	1	111686	F14L17	469229	28264	28266	SNP	1		C/G
5	AC012188	1	111686	F14L17	469230	28434	28436	SNP	1		C/T
5	AC012188	1	111686	F14L17	469641	12917	12921	IND	2	3/-3	
5	AC012188	1	111686	F14L17	469642	12994	12998	IND	2	3/-3	
5	AC012188	1	111686	F14L17	469643	25080	25081	IND	2	-3/3	
5	AC012188	1	111686	F14L17	469644	25362	25376	IND	2	13/-13	
5	AC012188	1	111686	F14L17	469645	53934	53939	IND	2	4/-4	
5	AC012188	1	111686	F14L17	469646	589	590	IND	2	-8/8	
5	AC012188	1	111686	F14L17	469647	7150	7169	IND	2	18/-18	
5	AC012188	1	111686	F14L17	471129	13218	13219	IND	1	-2/2	
5	AC012188	1	111686	F14L17	471130	13229	13231	IND	1	1/-1	
5	AC012188	1	111686	F14L17	471131	13241	13242	IND	1	-1/1	
5	AC012188	1	111686	F14L17	471132	13259	13260	IND	1	-2/2	
5	AC012188	1	111686	F14L17	471133	28090	28092	IND	1	1/-1	
5	AC012188	1	111686	F14L17	471134	52197	52198	IND	1	-1/1	
5	AC012188	1	111686	F14L17	471135	8237	8239	IND	1	1/-1	
6	AC013453	1	91001	T16N11	467167	28529	28531	SNP	1		C/T
6	AC013453	1	91001	T16N11	467255	19140	19142	SNP	1		C/G
6	AC013453	1	91001	T16N11	467267	10029	10031	SNP	1		C/T
6	AC013453	1	91001	T16N11	467501	57756	57758	SNP	1		A/G
6	AC013453	1	91001	T16N11	467783	17975	17977	SNP	1		G/C
6	AC013453	1	91001	T16N11	467784	17656	17658	SNP	1		A/C
6	AC013453	1	91001	T16N11	467785	17953	17955	SNP	1		A/T
6	AC013453	1	91001	T16N11	468021	34822	34824	SNP	1		T/G
6	AC013453	1	91001	T16N11	468268	63538	63540	SNP	1		G/A
6	AC013453	1	91001	T16N11	468269	63621	63623	SNP	1		C/A
6	AC013453	1	91001	T16N11	468398	69633	69635	SNP	1		G/A
6	AC013453	1	91001	T16N11	468399	69436	69438	SNP	1		A/T
6	AC013453	1	91001	T16N11	470620	1644	1645	IND	2	-62/62	
6	AC013453	1	91001	T16N11	470621	43319	43324	IND	2	4/-4	
6	AC013453	1	91001	T16N11	470622	4663	4664	IND	2	-3/3	
6	AC013453	1	91001	T16N11	470623	53383	53393	IND	2	9/-9	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
6	AC013453	1	91001	T16N11	470624	53807	53812	IND	2	4/-4	
6	AC013453	1	91001	T16N11	470625	54079	54080	IND	2	-9/9	
6	AC013453	1	91001	T16N11	470626	54245	54250	IND	2	4/-4	
6	AC013453	1	91001	T16N11	470627	61856	61857	IND	2	-3/3	
6	AC013453	1	91001	T16N11	470628	65845	65846	IND	2	-3/3	
6	AC013453	1	91001	T16N11	470629	73501	74185	IND	2	683/-683	
6	AC013453	1	91001	T16N11	470630	75366	75367	IND	2	-40/40	
6	AC013453	1	91001	T16N11	470631	785	824	IND	2	38/-38	
6	AC013453	1	91001	T16N11	470632	82376	82377	IND	2	-10/10	
6	AC013453	1	91001	T16N11	470633	83456	83457	IND	2	-4/4	
6	AC013453	1	91001	T16N11	470634	87652	87653	IND	2	-38/38	
6	AC013453	1	91001	T16N11	470635	89018	89022	IND	2	3/-3	
6	AC013453	1	91001	T16N11	470636	89440	89441	IND	2	-14/14	
6	AC013453	1	91001	T16N11	470637	89501	89502	IND	2	-7/7	
6	AC013453	1	91001	T16N11	470638	89517	89518	IND	2	-4/4	
6	AC013453	1	91001	T16N11	471445	17207	17209	IND	1	1/-1	
6	AC013453	1	91001	T16N11	471446	57919	57920	IND	1	-1/1	
6	AC013453	1	91001	T16N11	471447	58215	58217	IND	1	1/-1	
7	AC007843	1	84974	F28G4	471969	38690	38692	SNP	1		T/A
7	AC007843	1	84974	F28G4	471970	38649	38651	SNP	1		A/G
7	AC007843	1	84974	F28G4	471971	38942	38944	SNP	1		C/T
7	AC007843	1	84974	F28G4	471972	36515	36517	SNP	1		T/C
7	AC007843	1	84974	F28G4	472348	53346	53348	SNP	1		T/A
7	AC007843	1	84974	F28G4	472465	33221	33223	SNP	1		G/A
7	AC007843	1	84974	F28G4	472589	81782	81784	SNP	1		G/A
7	AC007843	1	84974	F28G4	472590	81750	81752	SNP	1		A/G
7	AC007843	1	84974	F28G4	473218	20427	20429	SNP	1		A/T
7	AC007843	1	84974	F28G4	473266	2791	2793	SNP	1		G/A
7	AC007843	1	84974	F28G4	473267	2665	2667	SNP	1		C/A
7	AC007843	1	84974	F28G4	473459	72436	72438	SNP	1		C/A
7	AC007843	1	84974	F28G4	473514	50798	50800	SNP	1		G/A
7	AC007843	1	84974	F28G4	473575	30692	30694	SNP	1		T/A
7	AC007843	1	84974	F28G4	473576	30797	30799	SNP	1		A/G
7	AC007843	1	84974	F28G4	473733	1050	1052	SNP	1		C/T
7	AC007843	1	84974	F28G4	473807	32248	32250	SNP	1		C/T
7	AC007843	1	84974	F28G4	474168	20447	20450	IND	1	2/-2	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
7	AC007843	1	84974	F28G4	474169	32465	32466	IND	1	-1/1	
7	AC007843	1	84974	F28G4	474170	38915	38916	IND	1	-3/3	
7	AC007843	1	84974	F28G4	474171	50805	50806	IND	1	-1/1	
7	AC007843	1	84974	F28G4	474172	63014	63016	IND	1	1/-1	
7	AC007843	1	84974	F28G4	474173	68446	68447	IND	1	-1/1	
7	AC007843	1	84974	F28G4	474174	74022	74023	IND	1	-5/5	
7	AC007843	1	84974	F28G4	474175	82176	82177	IND	1	-1/1	
8	AC013354	1	95327	F15H18	466842	10919	10921	SNP	1		T/C
8	AC013354	1	95327	F15H18	466843	11647	11649	SNP	1		G/A
8	AC013354	1	95327	F15H18	466844	11666	11668	SNP	1		A/G
8	AC013354	1	95327	F15H18	467047	88013	88015	SNP	1		T/C
8	AC013354	1	95327	F15H18	467102	28401	28403	SNP	1		G/A
8	AC013354	1	95327	F15H18	467103	28010	28012	SNP	1		T/C
8	AC013354	1	95327	F15H18	467104	28433	28435	SNP	1		C/G
8	AC013354	1	95327	F15H18	467137	75705	75707	SNP	1		A/G
8	AC013354	1	95327	F15H18	467172	50258	50260	SNP	1		C/A
8	AC013354	1	95327	F15H18	467173	50359	50361	SNP	1		G/A
8	AC013354	1	95327	F15H18	467174	49635	49637	SNP	1		A/G
8	AC013354	1	95327	F15H18	467329	86163	86165	SNP	1		A/G
8	AC013354	1	95327	F15H18	467419	51420	51422	SNP	1		A/T
8	AC013354	1	95327	F15H18	467536	13891	13893	SNP	1		A/G
8	AC013354	1	95327	F15H18	467537	13686	13688	SNP	1		A/G
8	AC013354	1	95327	F15H18	467949	61181	61183	SNP	1		G/A
8	AC013354	1	95327	F15H18	467950	60464	60466	SNP	1		T/C
8	AC013354	1	95327	F15H18	468099	24702	24704	SNP	1		T/A
8	AC013354	1	95327	F15H18	468360	59363	59365	SNP	1		C/T
8	AC013354	1	95327	F15H18	468366	17436	17438	SNP	1		C/T
8	AC013354	1	95327	F15H18	468527	80512	80514	SNP	1		T/A
8	AC013354	1	95327	F15H18	468528	80469	80471	SNP	1		G/A
8	AC013354	1	95327	F15H18	468529	80302	80304	SNP	1		C/A
8	AC013354	1	95327	F15H18	468530	80285	80287	SNP	1		T/C
8	AC013354	1	95327	F15H18	468531	80399	80401	SNP	1		A/T
8	AC013354	1	95327	F15H18	468836	89143	89145	SNP	1		G/A
8	AC013354	1	95327	F15H18	468837	89142	89144	SNP	1		T/C
8	AC013354	1	95327	F15H18	469110	25660	25662	SNP	1		C/A
8	AC013354	1	95327	F15H18	469686	33103	33107	IND	2	3/-3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
8	AC013354	1	95327	F15H18	469687	34119	34120	IND	2	-13/13	
8	AC013354	1	95327	F15H18	469688	34718	34719	IND	2	-5/5	
8	AC013354	1	95327	F15H18	469689	34728	34729	IND	2	-5/5	
8	AC013354	1	95327	F15H18	469690	34729	34730	IND	2	-5/5	
8	AC013354	1	95327	F15H18	469691	661	662	IND	2	-3/3	
8	AC013354	1	95327	F15H18	469692	69755	69756	IND	2	-76/76	
8	AC013354	1	95327	F15H18	469693	69999	70000	IND	2	-3/3	
8	AC013354	1	95327	F15H18	469694	93733	93740	IND	2	6/-6	
8	AC013354	1	95327	F15H18	471151	49807	49808	IND	1	-1/1	
8	AC013354	1	95327	F15H18	471152	51698	51699	IND	1	-1/1	
8	AC013354	1	95327	F15H18	471153	60963	60964	IND	1	-2/2	
8	AC013354	1	95327	F15H18	471154	62791	62793	IND	1	1/-1	
9	AC011809	1	108767	F6A14	466830	78434	78436	SNP	1		G/A
9	AC011809	1	108767	F6A14	467071	1725	1727	SNP	1		A/G
9	AC011809	1	108767	F6A14	467516	99378	99380	SNP	1		T/G
9	AC011809	1	108767	F6A14	467517	99588	99590	SNP	1		T/G
9	AC011809	1	108767	F6A14	467518	99630	99632	SNP	1		T/G
9	AC011809	1	108767	F6A14	467519	99629	99631	SNP	1		G/T
9	AC011809	1	108767	F6A14	467636	10625	10627	SNP	1		C/G
9	AC011809	1	108767	F6A14	467909	90918	90920	SNP	1		T/C
9	AC011809	1	108767	F6A14	467910	91261	91263	SNP	1		C/T
9	AC011809	1	108767	F6A14	467912	93641	93643	SNP	1		T/C
9	AC011809	1	108767	F6A14	467956	11981	11983	SNP	1		T/A
9	AC011809	1	108767	F6A14	467996	61143	61145	SNP	1		G/A
9	AC011809	1	108767	F6A14	468404	71034	71036	SNP	1		G/T
9	AC011809	1	108767	F6A14	468730	100765	100767	SNP	1		A/G
9	AC011809	1	108767	F6A14	468930	41772	41774	SNP	1		C/A
9	AC011809	1	108767	F6A14	468931	41838	41840	SNP	1		A/G
9	AC011809	1	108767	F6A14	468932	41792	41794	SNP	1		A/G
9	AC011809	1	108767	F6A14	468933	41790	41792	SNP	1		A/T
9	AC011809	1	108767	F6A14	469327	48681	48683	SNP	1		G/A
9	AC011809	1	108767	F6A14	469328	48035	48037	SNP	1		G/A
9	AC011809	1	108767	F6A14	469329	48011	48013	SNP	1		T/G
9	AC011809	1	108767	F6A14	469359	12695	12697	SNP	1		T/A
9	AC011809	1	108767	F6A14	469360	12710	12712	SNP	1		G/A
9	AC011809	1	108767	F6A14	469361	12856	12858	SNP	1		A/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
9	AC011809	1	108767	F6A14	469362	12750	12752	SNP	1		A/T
9	AC011809	1	108767	F6A14	469363	12883	12885	SNP	1		A/T
9	AC011809	1	108767	F6A14	470349	1228	1233	IND	2	4/-4	
9	AC011809	1	108767	F6A14	470350	17414	17420	IND	2	5/-5	
9	AC011809	1	108767	F6A14	470351	17539	17548	IND	2	8/-8	
9	AC011809	1	108767	F6A14	470352	19481	19487	IND	2	5/-5	
9	AC011809	1	108767	F6A14	470353	19484	19490	IND	2	5/-5	
9	AC011809	1	108767	F6A14	470354	26341	26342	IND	2	-4/4	
9	AC011809	1	108767	F6A14	470355	29069	29070	IND	2	-5/5	
9	AC011809	1	108767	F6A14	470356	3626	3634	IND	2	7/-7	
9	AC011809	1	108767	F6A14	470357	41742	41746	IND	2	3/-3	
9	AC011809	1	108767	F6A14	470358	49745	49772	IND	2	26/-26	
9	AC011809	1	108767	F6A14	470359	51376	51391	IND	2	14/-14	
9	AC011809	1	108767	F6A14	470360	52572	52587	IND	2	14/-14	
9	AC011809	1	108767	F6A14	470361	67267	67268	IND	2	-21/21	
9	AC011809	1	108767	F6A14	470362	69171	69172	IND	2	-7/7	
9	AC011809	1	108767	F6A14	470363	69305	69309	IND	2	3/-3	
9	AC011809	1	108767	F6A14	470364	69409	69413	IND	2	3/-3	
9	AC011809	1	108767	F6A14	470365	72544	72592	IND	2	47/-47	
9	AC011809	1	108767	F6A14	470366	72701	72702	IND	2	-4/4	
9	AC011809	1	108767	F6A14	470367	79629	79638	IND	2	8/-8	
9	AC011809	1	108767	F6A14	470368	79720	79735	IND	2	14/-14	
9	AC011809	1	108767	F6A14	470369	80790	80807	IND	2	16/-16	
9	AC011809	1	108767	F6A14	470370	80929	80935	IND	2	5/-5	
9	AC011809	1	108767	F6A14	470371	81547	81548	IND	2	-8/8	
9	AC011809	1	108767	F6A14	470372	82685	82702	IND	2	16/-16	
9	AC011809	1	108767	F6A14	470373	83457	83461	IND	2	3/-3	
9	AC011809	1	108767	F6A14	470374	84372	84373	IND	2	-5/5	
9	AC011809	1	108767	F6A14	471351	26346	26347	IND	1	-2/2	
9	AC011809	1	108767	F6A14	471352	35005	35006	IND	1	-1/1	
9	AC011809	1	108767	F6A14	471353	41748	41752	IND	1	3/-3	
9	AC011809	1	108767	F6A14	471354	41841	41843	IND	1	1/-1	
9	AC011809	1	108767	F6A14	471355	70952	70953	IND	1	-1/1	
9	AC011809	1	108767	F6A14	471356	71084	71085	IND	1	-1/1	
9	AC011809	1	108767	F6A14	471357	89198	89200	IND	1	1/-1	
10	AC007797	1	119942	F6F9	472001	33213	33215	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
10	AC007797	1	119942	F6F9	472026	31294	31296	SNP	1		C/T
10	AC007797	1	119942	F6F9	472281	109304	109306	SNP	1		G/A
10	AC007797	1	119942	F6F9	472282	108719	108721	SNP	1		A/G
10	AC007797	1	119942	F6F9	472340	13283	13285	SNP	1		C/T
10	AC007797	1	119942	F6F9	472341	28434	28436	SNP	1		A/C
10	AC007797	1	119942	F6F9	472342	28251	28253	SNP	1		A/C
10	AC007797	1	119942	F6F9	472343	28568	28570	SNP	1		T/G
10	AC007797	1	119942	F6F9	472405	52872	52874	SNP	1		A/T
10	AC007797	1	119942	F6F9	472418	59390	59392	SNP	1		G/T
10	AC007797	1	119942	F6F9	472419	39439	39441	SNP	1		T/C
10	AC007797	1	119942	F6F9	472764	45349	45351	SNP	1		A/T
10	AC007797	1	119942	F6F9	472765	45348	45350	SNP	1		A/T
10	AC007797	1	119942	F6F9	472790	3652	3654	SNP	1		T/A
10	AC007797	1	119942	F6F9	472791	19498	19500	SNP	1		G/T
10	AC007797	1	119942	F6F9	472797	35106	35108	SNP	1		T/C
10	AC007797	1	119942	F6F9	472804	50550	50552	SNP	1		C/A
10	AC007797	1	119942	F6F9	472805	50614	50616	SNP	1		C/A
10	AC007797	1	119942	F6F9	472806	50719	50721	SNP	1		G/A
10	AC007797	1	119942	F6F9	472807	50799	50801	SNP	1		T/A
10	AC007797	1	119942	F6F9	472808	50549	50551	SNP	1		A/C
10	AC007797	1	119942	F6F9	472809	50680	50682	SNP	1		T/G
10	AC007797	1	119942	F6F9	472810	50956	50958	SNP	1		A/G
10	AC007797	1	119942	F6F9	472811	50525	50527	SNP	1		C/T
10	AC007797	1	119942	F6F9	473122	76749	76751	SNP	1		G/A
10	AC007797	1	119942	F6F9	473123	76404	76406	SNP	1		C/A
10	AC007797	1	119942	F6F9	473124	76466	76468	SNP	1		C/T
10	AC007797	1	119942	F6F9	473162	71610	71612	SNP	1		T/A
10	AC007797	1	119942	F6F9	473279	22853	22855	SNP	1		G/A
10	AC007797	1	119942	F6F9	473280	23986	23988	SNP	1		T/C
10	AC007797	1	119942	F6F9	473355	26840	26842	SNP	1		G/C
10	AC007797	1	119942	F6F9	473356	26839	26841	SNP	1		A/T
10	AC007797	1	119942	F6F9	473707	22291	22293	SNP	1		T/A
10	AC007797	1	119942	F6F9	473708	21992	21994	SNP	1		C/T
10	AC007797	1	119942	F6F9	473923	1378	1379	IND	2	-3/3	
10	AC007797	1	119942	F6F9	473924	1636	1646	IND	2	9/-9	
10	AC007797	1	119942	F6F9	474273	24162	24169	IND	1	6/-6	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
10	AC007797	1	119942	F6F9	474274	45596	45597	IND	1	-1/1	
10	AC007797	1	119942	F6F9	474275	50570	50572	IND	1	1/-1	
10	AC007797	1	119942	F6F9	474276	50800	50802	IND	1	1/-1	
10	AC007797	1	119942	F6F9	474277	71576	71577	IND	1	-1/1	
11	AC012190	1	68986	T22I11	466902	45547	45549	SNP	1		G/C
11	AC012190	1	68986	T22I11	466903	45145	45147	SNP	1		C/G
11	AC012190	1	68986	T22I11	467340	4236	4238	SNP	1		G/A
11	AC012190	1	68986	T22I11	467341	4237	4239	SNP	1		T/C
11	AC012190	1	68986	T22I11	467342	4056	4058	SNP	1		A/T
11	AC012190	1	68986	T22I11	468248	36570	36572	SNP	1		T/A
11	AC012190	1	68986	T22I11	469064	31729	31731	SNP	1		G/A
11	AC012190	1	68986	T22I11	469065	31716	31718	SNP	1		C/A
11	AC012190	1	68986	T22I11	469066	31679	31681	SNP	1		G/A
11	AC012190	1	68986	T22I11	469067	31664	31666	SNP	1		G/A
11	AC012190	1	68986	T22I11	469068	31575	31577	SNP	1		T/C
11	AC012190	1	68986	T22I11	469069	31714	31716	SNP	1		G/T
11	AC012190	1	68986	T22I11	469070	31680	31682	SNP	1		A/T
11	AC012190	1	68986	T22I11	469181	33287	33289	SNP	1		T/A
11	AC012190	1	68986	T22I11	469182	33300	33302	SNP	1		A/C
11	AC012190	1	68986	T22I11	470825	16066	16067	IND	2	-5/5	
11	AC012190	1	68986	T22I11	470826	16067	16068	IND	2	-5/5	
11	AC012190	1	68986	T22I11	470827	25184	28287	IND	2	3102/-3102	
11	AC012190	1	68986	T22I11	470828	25247	28349	IND	2	3101/-3101	
11	AC012190	1	68986	T22I11	470829	33224	33225	IND	2	-3/3	
11	AC012190	1	68986	T22I11	470830	34492	34493	IND	2	-3/3	
11	AC012190	1	68986	T22I11	470831	34608	34609	IND	2	-6/6	
11	AC012190	1	68986	T22I11	470832	41387	41402	IND	2	14/-14	
11	AC012190	1	68986	T22I11	470833	62114	62144	IND	2	29/-29	
11	AC012190	1	68986	T22I11	470834	62115	62145	IND	2	29/-29	
11	AC012190	1	68986	T22I11	471534	3797	3798	IND	1	-1/1	
11	AC012190	1	68986	T22I11	471535	38618	38619	IND	1	-2/2	
12	AC015447	1	108365	F24J8	471693	41663	41665	SNP	1		A/T
12	AC015447	1	108365	F24J8	471937	43452	43454	SNP	1		G/A
12	AC015447	1	108365	F24J8	472249	21555	21557	SNP	1		C/A
12	AC015447	1	108365	F24J8	472250	21629	21631	SNP	1		A/G
12	AC015447	1	108365	F24J8	472427	54381	54383	SNP	1		G/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
12	AC015447	1	108365	F24J8	472428	54336	54338	SNP	1		T/C
12	AC015447	1	108365	F24J8	472700	9506	9508	SNP	1		G/A
12	AC015447	1	108365	F24J8	472946	428	430	SNP	1		T/A
12	AC015447	1	108365	F24J8	472947	370	372	SNP	1		T/C
12	AC015447	1	108365	F24J8	472948	1161	1163	SNP	1		G/T
12	AC015447	1	108365	F24J8	472971	7857	7859	SNP	1		G/C
12	AC015447	1	108365	F24J8	473018	97725	97727	SNP	1		G/A
12	AC015447	1	108365	F24J8	473069	81701	81703	SNP	1		C/G
12	AC015447	1	108365	F24J8	473074	39366	39368	SNP	1		G/A
12	AC015447	1	108365	F24J8	473075	39821	39823	SNP	1		T/C
12	AC015447	1	108365	F24J8	473076	41084	41086	SNP	1		A/C
12	AC015447	1	108365	F24J8	473077	39866	39868	SNP	1		A/G
12	AC015447	1	108365	F24J8	473078	40293	40295	SNP	1		A/G
12	AC015447	1	108365	F24J8	473079	40912	40914	SNP	1		T/G
12	AC015447	1	108365	F24J8	473080	41342	41344	SNP	1		A/G
12	AC015447	1	108365	F24J8	473081	39252	39254	SNP	1		A/G
12	AC015447	1	108365	F24J8	473082	39363	39365	SNP	1		A/G
12	AC015447	1	108365	F24J8	473083	39407	39409	SNP	1		A/G
12	AC015447	1	108365	F24J8	473084	39904	39906	SNP	1		C/T
12	AC015447	1	108365	F24J8	473333	55348	55350	SNP	1		T/A
12	AC015447	1	108365	F24J8	473334	55866	55868	SNP	1		A/G
12	AC015447	1	108365	F24J8	473359	18971	18973	SNP	1		C/A
12	AC015447	1	108365	F24J8	473448	11020	11022	SNP	1		C/A
12	AC015447	1	108365	F24J8	473706	16316	16318	SNP	1		G/A
12	AC015447	1	108365	F24J8	473800	88375	88377	SNP	1		T/A
12	AC015447	1	108365	F24J8	473801	88137	88139	SNP	1		A/G
12	AC015447	1	108365	F24J8	473876	1713	1714	IND	2	-5/5	
12	AC015447	1	108365	F24J8	473877	2950	2951	IND	2	-3/3	
12	AC015447	1	108365	F24J8	473878	3799	3809	IND	2	9/-9	
12	AC015447	1	108365	F24J8	474151	21780	21782	IND	1	1/-1	
12	AC015447	1	108365	F24J8	474152	21790	21792	IND	1	1/-1	
12	AC015447	1	108365	F24J8	474153	54578	54580	IND	1	1/-1	
12	AC015447	1	108365	F24J8	474154	54580	54582	IND	1	1/-1	
12	AC015447	1	108365	F24J8	474155	88477	88479	IND	1	1/-1	
13	AC013482	1	82875	T26F17	466960	80054	80056	SNP	1		T/A
13	AC013482	1	82875	T26F17	467546	38141	38143	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
13	AC013482	1	82875	T26F17	467547	38129	38131	SNP	1		T/C
13	AC013482	1	82875	T26F17	467548	38271	38273	SNP	1		C/T
13	AC013482	1	82875	T26F17	467599	68893	68895	SNP	1		C/A
13	AC013482	1	82875	T26F17	467600	68916	68918	SNP	1		T/C
13	AC013482	1	82875	T26F17	467873	39174	39176	SNP	1		T/C
13	AC013482	1	82875	T26F17	467937	50413	50415	SNP	1		G/A
13	AC013482	1	82875	T26F17	467938	50076	50078	SNP	1		T/C
13	AC013482	1	82875	T26F17	468489	17848	17850	SNP	1		C/A
13	AC013482	1	82875	T26F17	468490	17993	17995	SNP	1		C/T
13	AC013482	1	82875	T26F17	468491	13241	13243	SNP	1		A/G
13	AC013482	1	82875	T26F17	468492	14581	14583	SNP	1		T/A
13	AC013482	1	82875	T26F17	468493	14563	14565	SNP	1		T/A
13	AC013482	1	82875	T26F17	468494	16646	16648	SNP	1		G/C
13	AC013482	1	82875	T26F17	468495	15924	15926	SNP	1		A/G
13	AC013482	1	82875	T26F17	468496	14620	14622	SNP	1		A/T
13	AC013482	1	82875	T26F17	468497	14568	14570	SNP	1		A/T
13	AC013482	1	82875	T26F17	468498	16097	16099	SNP	1		C/T
13	AC013482	1	82875	T26F17	468533	5138	5140	SNP	1		A/C
13	AC013482	1	82875	T26F17	468534	5082	5084	SNP	1		G/T
13	AC013482	1	82875	T26F17	468535	5083	5085	SNP	1		C/T
13	AC013482	1	82875	T26F17	468554	48137	48139	SNP	1		A/T
13	AC013482	1	82875	T26F17	469195	52136	52138	SNP	1		T/C
13	AC013482	1	82875	T26F17	470857	11723	11724	IND	2	-5/5	
13	AC013482	1	82875	T26F17	470858	15917	15918	IND	2	-4/4	
13	AC013482	1	82875	T26F17	470859	15941	15942	IND	2	-3/3	
13	AC013482	1	82875	T26F17	470860	36132	36133	IND	2	-4/4	
13	AC013482	1	82875	T26F17	470861	39858	39862	IND	2	3/-3	
13	AC013482	1	82875	T26F17	470862	48265	48269	IND	2	3/-3	
13	AC013482	1	82875	T26F17	470863	65258	65495	IND	2	236/-236	
13	AC013482	1	82875	T26F17	470864	65260	65497	IND	2	236/-236	
13	AC013482	1	82875	T26F17	470865	71109	71656	IND	2	546/-546	
13	AC013482	1	82875	T26F17	470866	72094	72095	IND	2	-6/6	
13	AC013482	1	82875	T26F17	470867	72390	72391	IND	2	-8/8	
13	AC013482	1	82875	T26F17	470868	7476	7477	IND	2	-3/3	
13	AC013482	1	82875	T26F17	470869	74927	74964	IND	2	36/-36	
13	AC013482	1	82875	T26F17	470870	77554	77559	IND	2	4/-4	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
13	AC013482	1	82875	T26F17	470871	77583	77588	IND	2	4/-4	
13	AC013482	1	82875	T26F17	470872	78801	78802	IND	2	-3/3	
13	AC013482	1	82875	T26F17	470873	78962	78963	IND	2	-8/8	
13	AC013482	1	82875	T26F17	471543	14572	14573	IND	1	-1/1	
13	AC013482	1	82875	T26F17	471544	14582	14584	IND	1	1/-1	
13	AC013482	1	82875	T26F17	471545	15920	15921	IND	1	-4/4	
13	AC013482	1	82875	T26F17	471546	15949	15950	IND	1	-3/3	
13	AC013482	1	82875	T26F17	471547	26078	26080	IND	1	1/-1	
13	AC013482	1	82875	T26F17	471548	39362	39364	IND	1	1/-1	
13	AC013482	1	82875	T26F17	471549	39861	39864	IND	1	2/-2	
13	AC013482	1	82875	T26F17	471550	39865	39867	IND	1	1/-1	
13	AC013482	1	82875	T26F17	471551	48265	48268	IND	1	2/-2	
13	AC013482	1	82875	T26F17	471552	48268	48270	IND	1	1/-1	
13	AC013482	1	82875	T26F17	471553	68895	68896	IND	1	-4/4	
13	AC013482	1	82875	T26F17	471554	7085	7086	IND	1	-2/2	
14	AC013427	1	89473	T1K7	471730	54814	54816	SNP	1		G/A
14	AC013427	1	89473	T1K7	471756	66530	66532	SNP	1		C/A
14	AC013427	1	89473	T1K7	471757	66052	66054	SNP	1		G/A
14	AC013427	1	89473	T1K7	471758	65683	65685	SNP	1		T/C
14	AC013427	1	89473	T1K7	471759	66533	66535	SNP	1		A/G
14	AC013427	1	89473	T1K7	471935	55500	55502	SNP	1		T/A
14	AC013427	1	89473	T1K7	471936	55321	55323	SNP	1		A/T
14	AC013427	1	89473	T1K7	472331	67252	67254	SNP	1		T/C
14	AC013427	1	89473	T1K7	472588	79950	79952	SNP	1		G/A
14	AC013427	1	89473	T1K7	472758	34006	34008	SNP	1		C/T
14	AC013427	1	89473	T1K7	472759	20668	20670	SNP	1		C/T
14	AC013427	1	89473	T1K7	472760	19753	19755	SNP	1		A/G
14	AC013427	1	89473	T1K7	472761	19123	19125	SNP	1		A/G
14	AC013427	1	89473	T1K7	472788	68176	68178	SNP	1		T/G
14	AC013427	1	89473	T1K7	472789	68132	68134	SNP	1		G/T
14	AC013427	1	89473	T1K7	472870	83185	83187	SNP	1		T/C
14	AC013427	1	89473	T1K7	473320	81290	81292	SNP	1		A/G
14	AC013427	1	89473	T1K7	473679	37905	37907	SNP	1		G/A
14	AC013427	1	89473	T1K7	473680	37751	37753	SNP	1		T/A
14	AC013427	1	89473	T1K7	474005	21862	21863	IND	2	-3/3	
14	AC013427	1	89473	T1K7	474006	5731	5732	IND	2	-6/6	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
14	AC013427	1	89473	T1K7	474408	29407	29409	IND	1	1/-1	
14	AC013427	1	89473	T1K7	474409	29409	29411	IND	1	1/-1	
14	AC013427	1	89473	T1K7	474410	38823	38825	IND	1	1/-1	
14	AC013427	1	89473	T1K7	474411	5748	5749	IND	1	-1/1	
14	AC013427	1	89473	T1K7	474412	5750	5751	IND	1	-5/5	
14	AC013427	1	89473	T1K7	474413	68076	68078	IND	1	1/-1	
15	AC012375	1	106753	T22C5	466845	45167	45169	SNP	1		T/C
15	AC012375	1	106753	T22C5	466846	44293	44295	SNP	1		G/A
15	AC012375	1	106753	T22C5	466847	44358	44360	SNP	1		T/C
15	AC012375	1	106753	T22C5	466848	44076	44078	SNP	1		T/G
15	AC012375	1	106753	T22C5	466849	44091	44093	SNP	1		G/T
15	AC012375	1	106753	T22C5	467088	78195	78197	SNP	1		C/T
15	AC012375	1	106753	T22C5	467194	49204	49206	SNP	1		C/T
15	AC012375	1	106753	T22C5	467195	50897	50899	SNP	1		G/T
15	AC012375	1	106753	T22C5	467724	39952	39954	SNP	1		C/A
15	AC012375	1	106753	T22C5	467725	40340	40342	SNP	1		A/T
15	AC012375	1	106753	T22C5	467757	38305	38307	SNP	1		C/G
15	AC012375	1	106753	T22C5	467849	74111	74113	SNP	1		G/T
15	AC012375	1	106753	T22C5	468251	79655	79657	SNP	1		T/A
15	AC012375	1	106753	T22C5	468870	70425	70427	SNP	1		G/A
15	AC012375	1	106753	T22C5	468871	71351	71353	SNP	1		A/G
15	AC012375	1	106753	T22C5	468872	70755	70757	SNP	1		A/G
15	AC012375	1	106753	T22C5	469192	51953	51955	SNP	1		T/A
15	AC012375	1	106753	T22C5	469193	51952	51954	SNP	1		G/A
15	AC012375	1	106753	T22C5	469196	76885	76887	SNP	1		A/G
15	AC012375	1	106753	T22C5	469197	76715	76717	SNP	1		A/G
15	AC012375	1	106753	T22C5	469198	76881	76883	SNP	1		C/T
15	AC012375	1	106753	T22C5	469246	105247	105249	SNP	1		C/G
15	AC012375	1	106753	T22C5	469247	105141	105143	SNP	1		A/G
15	AC012375	1	106753	T22C5	470767	102330	103153	IND	2	822/-822	
15	AC012375	1	106753	T22C5	470768	102773	102774	IND	2	-10/10	
15	AC012375	1	106753	T22C5	470769	102996	102997	IND	2	-9/9	
15	AC012375	1	106753	T22C5	470770	102998	102999	IND	2	-9/9	
15	AC012375	1	106753	T22C5	470771	3018	3030	IND	2	11/-11	
15	AC012375	1	106753	T22C5	470772	34261	34265	IND	2	3/-3	
15	AC012375	1	106753	T22C5	470773	3752	3757	IND	2	4/-4	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
15	AC012375	1	106753	T22C5	470774	3765	3766	IND	2	-4/4	
15	AC012375	1	106753	T22C5	470775	3766	3767	IND	2	-4/4	
15	AC012375	1	106753	T22C5	470776	40488	40489	IND	2	-3/3	
15	AC012375	1	106753	T22C5	470777	46971	46979	IND	2	7/-7	
15	AC012375	1	106753	T22C5	470778	48103	48108	IND	2	4/-4	
15	AC012375	1	106753	T22C5	470779	73988	73994	IND	2	5/-5	
15	AC012375	1	106753	T22C5	470780	88701	88705	IND	2	3/-3	
15	AC012375	1	106753	T22C5	470781	88744	88745	IND	2	-5/5	
15	AC012375	1	106753	T22C5	470782	88879	88912	IND	2	32/-32	
15	AC012375	1	106753	T22C5	470783	88879	88944	IND	2	64/-64	
15	AC012375	1	106753	T22C5	470784	88913	88978	IND	2	64/-64	
15	AC012375	1	106753	T22C5	470785	92763	92764	IND	2	-9/9	
15	AC012375	1	106753	T22C5	470786	92768	92769	IND	2	-9/9	
15	AC012375	1	106753	T22C5	470787	93017	93018	IND	2	-8/8	
15	AC012375	1	106753	T22C5	470788	93018	93019	IND	2	-9/9	
15	AC012375	1	106753	T22C5	470789	93019	93020	IND	2	-9/9	
15	AC012375	1	106753	T22C5	470790	93126	94398	IND	2	1271/-1271	
15	AC012375	1	106753	T22C5	470791	97594	97600	IND	2	5/-5	
15	AC012375	1	106753	T22C5	470792	99063	99969	IND	2	905/-905	
15	AC012375	1	106753	T22C5	471511	40490	40491	IND	1	-3/3	
15	AC012375	1	106753	T22C5	471512	52422	52423	IND	1	-1/1	
15	AC012375	1	106753	T22C5	471513	73913	73914	IND	1	-2/2	
15	AC012375	1	106753	T22C5	471514	73988	73990	IND	1	1/-1	
15	AC012375	1	106753	T22C5	471515	73990	73993	IND	1	2/-2	
15	AC012375	1	106753	T22C5	471516	73993	73996	IND	1	2/-2	
15	AC012375	1	106753	T22C5	471517	80252	80254	IND	1	1/-1	
16	AC010155	1	104163	F3M18	466986	78930	78932	SNP	1		T/A
16	AC010155	1	104163	F3M18	466987	79395	79397	SNP	1		G/C
16	AC010155	1	104163	F3M18	466988	79009	79011	SNP	1		T/C
16	AC010155	1	104163	F3M18	466989	78929	78931	SNP	1		A/C
16	AC010155	1	104163	F3M18	466990	79146	79148	SNP	1		A/G
16	AC010155	1	104163	F3M18	467048	75456	75458	SNP	1		G/A
16	AC010155	1	104163	F3M18	467089	7908	7910	SNP	1		T/C
16	AC010155	1	104163	F3M18	467090	7921	7923	SNP	1		T/G
16	AC010155	1	104163	F3M18	467091	8541	8543	SNP	1		A/G
16	AC010155	1	104163	F3M18	467092	10547	10549	SNP	1		T/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
16	AC010155	1	104163	F3M18	467093	10695	10697	SNP	1		C/T
16	AC010155	1	104163	F3M18	467225	76529	76531	SNP	1		T/A
16	AC010155	1	104163	F3M18	467226	77225	77227	SNP	1		A/G
16	AC010155	1	104163	F3M18	467477	60551	60553	SNP	1		A/C
16	AC010155	1	104163	F3M18	467478	60289	60291	SNP	1		C/T
16	AC010155	1	104163	F3M18	467479	60076	60078	SNP	1		C/T
16	AC010155	1	104163	F3M18	467480	61426	61428	SNP	1		A/T
16	AC010155	1	104163	F3M18	467481	62432	62434	SNP	1		T/A
16	AC010155	1	104163	F3M18	467482	63351	63353	SNP	1		T/C
16	AC010155	1	104163	F3M18	467483	63197	63199	SNP	1		G/C
16	AC010155	1	104163	F3M18	467484	63329	63331	SNP	1		C/G
16	AC010155	1	104163	F3M18	467485	62375	62377	SNP	1		A/T
16	AC010155	1	104163	F3M18	467841	56888	56890	SNP	1		G/A
16	AC010155	1	104163	F3M18	467842	57075	57077	SNP	1		A/C
16	AC010155	1	104163	F3M18	467843	57375	57377	SNP	1		T/C
16	AC010155	1	104163	F3M18	467844	58013	58015	SNP	1		A/T
16	AC010155	1	104163	F3M18	467845	57315	57317	SNP	1		G/T
16	AC010155	1	104163	F3M18	467904	44898	44900	SNP	1		A/G
16	AC010155	1	104163	F3M18	467905	44960	44962	SNP	1		C/T
16	AC010155	1	104163	F3M18	468012	97537	97539	SNP	1		A/C
16	AC010155	1	104163	F3M18	468013	96987	96989	SNP	1		T/C
16	AC010155	1	104163	F3M18	468101	98404	98406	SNP	1		C/T
16	AC010155	1	104163	F3M18	468102	98403	98405	SNP	1		C/T
16	AC010155	1	104163	F3M18	468389	90835	90837	SNP	1		G/C
16	AC010155	1	104163	F3M18	468390	91321	91323	SNP	1		T/G
16	AC010155	1	104163	F3M18	468880	55307	55309	SNP	1		G/C
16	AC010155	1	104163	F3M18	468881	56174	56176	SNP	1		T/C
16	AC010155	1	104163	F3M18	469149	69097	69099	SNP	1		G/A
16	AC010155	1	104163	F3M18	469150	66193	66195	SNP	1		G/A
16	AC010155	1	104163	F3M18	469151	65628	65630	SNP	1		T/A
16	AC010155	1	104163	F3M18	469152	66770	66772	SNP	1		G/C
16	AC010155	1	104163	F3M18	469153	66213	66215	SNP	1		T/C
16	AC010155	1	104163	F3M18	469154	66577	66579	SNP	1		T/G
16	AC010155	1	104163	F3M18	469155	67030	67032	SNP	1		C/G
16	AC010155	1	104163	F3M18	469156	65834	65836	SNP	1		A/T
16	AC010155	1	104163	F3M18	469268	94804	94806	SNP	1		G/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
16	AC010155	1	104163	F3M18	469269	95460	95462	SNP	1		T/C
16	AC010155	1	104163	F3M18	469270	94867	94869	SNP	1		T/C
16	AC010155	1	104163	F3M18	470267	15913	15914	IND	2	-3/3	
16	AC010155	1	104163	F3M18	470268	21293	23958	IND	2	2664/-2664	
16	AC010155	1	104163	F3M18	470269	29833	29837	IND	2	3/-3	
16	AC010155	1	104163	F3M18	470270	45681	45686	IND	2	4/-4	
16	AC010155	1	104163	F3M18	470271	46209	46220	IND	2	10/-10	
16	AC010155	1	104163	F3M18	470272	53858	53859	IND	2	-11/11	
16	AC010155	1	104163	F3M18	470273	62645	62646	IND	2	-3/3	
16	AC010155	1	104163	F3M18	470274	68681	68688	IND	2	6/-6	
16	AC010155	1	104163	F3M18	470275	72674	72675	IND	2	-23/23	
16	AC010155	1	104163	F3M18	470276	87256	87257	IND	2	-6/6	
16	AC010155	1	104163	F3M18	470277	87824	87832	IND	2	7/-7	
16	AC010155	1	104163	F3M18	471329	31101	31103	IND	1	1/-1	
16	AC010155	1	104163	F3M18	471330	55218	55220	IND	1	1/-1	
16	AC010155	1	104163	F3M18	471331	69182	69183	IND	1	-1/1	
16	AC010155	1	104163	F3M18	471332	69194	69196	IND	1	1/-1	
17	AC021043	1	154716	F28N24	471748	61403	61405	SNP	1		A/C
17	AC021043	1	154716	F28N24	471749	61458	61460	SNP	1		T/C
17	AC021043	1	154716	F28N24	471750	61834	61836	SNP	1		C/G
17	AC021043	1	154716	F28N24	471751	61806	61808	SNP	1		C/T
17	AC021043	1	154716	F28N24	471785	113788	113790	SNP	1		T/G
17	AC021043	1	154716	F28N24	471786	114404	114406	SNP	1		C/T
17	AC021043	1	154716	F28N24	471854	89441	89443	SNP	1		C/A
17	AC021043	1	154716	F28N24	471855	89458	89460	SNP	1		A/T
17	AC021043	1	154716	F28N24	471856	89279	89281	SNP	1		A/T
17	AC021043	1	154716	F28N24	471957	64439	64441	SNP	1		G/T
17	AC021043	1	154716	F28N24	472027	115704	115706	SNP	1		G/A
17	AC021043	1	154716	F28N24	472028	115879	115881	SNP	1		T/C
17	AC021043	1	154716	F28N24	472070	81714	81716	SNP	1		A/G
17	AC021043	1	154716	F28N24	472256	124360	124362	SNP	1		C/G
17	AC021043	1	154716	F28N24	472257	124653	124655	SNP	1		T/G
17	AC021043	1	154716	F28N24	472258	124705	124707	SNP	1		C/T
17	AC021043	1	154716	F28N24	472526	96427	96429	SNP	1		T/A
17	AC021043	1	154716	F28N24	472527	96133	96135	SNP	1		A/G
17	AC021043	1	154716	F28N24	472528	96400	96402	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
17	AC021043	1	154716	F28N24	472542	48845	48847	SNP	1		T/C
17	AC021043	1	154716	F28N24	472543	48909	48911	SNP	1		A/G
17	AC021043	1	154716	F28N24	473127	58531	58533	SNP	1		A/G
17	AC021043	1	154716	F28N24	473192	49472	49474	SNP	1		G/A
17	AC021043	1	154716	F28N24	473193	49608	49610	SNP	1		A/G
17	AC021043	1	154716	F28N24	473454	83519	83521	SNP	1		G/A
17	AC021043	1	154716	F28N24	473557	100157	100159	SNP	1		G/A
17	AC021043	1	154716	F28N24	473558	100305	100307	SNP	1		T/A
17	AC021043	1	154716	F28N24	473559	100178	100180	SNP	1		G/C
17	AC021043	1	154716	F28N24	474183	10375	10376	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474184	10381	10383	IND	1	1/-1	
17	AC021043	1	154716	F28N24	474185	13369	13372	IND	1	2/-2	
17	AC021043	1	154716	F28N24	474186	19559	19561	IND	1	1/-1	
17	AC021043	1	154716	F28N24	474187	38585	38587	IND	1	1/-1	
17	AC021043	1	154716	F28N24	474188	49404	49405	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474189	69487	69494	IND	1	6/-6	
17	AC021043	1	154716	F28N24	474190	89351	89352	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474191	89352	89353	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474192	89353	89354	IND	1	-4/4	
17	AC021043	1	154716	F28N24	474193	89405	89406	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474194	90872	90873	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474195	90926	90927	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474196	90927	90928	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474197	96402	96407	IND	1	4/-4	
17	AC021043	1	154716	F28N24	474198	96494	96496	IND	1	1/-1	
17	AC021043	1	154716	F28N24	474199	97504	97505	IND	1	-1/1	
17	AC021043	1	154716	F28N24	474200	97587	97589	IND	1	1/-1	
17	AC021043	1	154716	F28N24	474201	99881	99883	IND	1	1/-1	
18	AC007767	1	127462	F5D14	471676	28152	28154	SNP	1		A/G
18	AC007767	1	127462	F5D14	471677	28226	28228	SNP	1		A/G
18	AC007767	1	127462	F5D14	471830	46452	46454	SNP	1		T/A
18	AC007767	1	127462	F5D14	471835	2248	2250	SNP	1		C/T
18	AC007767	1	127462	F5D14	471908	13356	13358	SNP	1		G/A
18	AC007767	1	127462	F5D14	471909	13419	13421	SNP	1		G/A
18	AC007767	1	127462	F5D14	471910	13378	13380	SNP	1		T/C
18	AC007767	1	127462	F5D14	471911	13183	13185	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
18	AC007767	1	127462	F5D14	471912	13175	13177	SNP	1		A/T
18	AC007767	1	127462	F5D14	471913	13377	13379	SNP	1		G/T
18	AC007767	1	127462	F5D14	471949	65926	65928	SNP	1		G/A
18	AC007767	1	127462	F5D14	471950	65670	65672	SNP	1		G/C
18	AC007767	1	127462	F5D14	471951	65615	65617	SNP	1		T/C
18	AC007767	1	127462	F5D14	472121	24933	24935	SNP	1		C/T
18	AC007767	1	127462	F5D14	472122	24917	24919	SNP	1		C/T
18	AC007767	1	127462	F5D14	472314	63958	63960	SNP	1		G/A
18	AC007767	1	127462	F5D14	472315	64442	64444	SNP	1		T/C
18	AC007767	1	127462	F5D14	472316	64140	64142	SNP	1		A/T
18	AC007767	1	127462	F5D14	472389	126438	126440	SNP	1		C/T
18	AC007767	1	127462	F5D14	472988	41743	41745	SNP	1		G/T
18	AC007767	1	127462	F5D14	473051	37145	37147	SNP	1		T/A
18	AC007767	1	127462	F5D14	473052	34838	34840	SNP	1		T/A
18	AC007767	1	127462	F5D14	473053	34840	34842	SNP	1		G/A
18	AC007767	1	127462	F5D14	473054	34848	34850	SNP	1		T/A
18	AC007767	1	127462	F5D14	473055	34850	34852	SNP	1		T/A
18	AC007767	1	127462	F5D14	473056	36705	36707	SNP	1		T/C
18	AC007767	1	127462	F5D14	473057	34839	34841	SNP	1		T/C
18	AC007767	1	127462	F5D14	473058	34844	34846	SNP	1		A/G
18	AC007767	1	127462	F5D14	473059	37186	37188	SNP	1		A/T
18	AC007767	1	127462	F5D14	473060	34842	34844	SNP	1		A/T
18	AC007767	1	127462	F5D14	473061	34845	34847	SNP	1		C/T
18	AC007767	1	127462	F5D14	473121	39496	39498	SNP	1		T/C
18	AC007767	1	127462	F5D14	473487	76301	76303	SNP	1		C/T
18	AC007767	1	127462	F5D14	473488	76593	76595	SNP	1		G/T
18	AC007767	1	127462	F5D14	473528	95186	95188	SNP	1		T/C
18	AC007767	1	127462	F5D14	473577	16395	16397	SNP	1		C/A
18	AC007767	1	127462	F5D14	473578	16959	16961	SNP	1		A/G
18	AC007767	1	127462	F5D14	473702	21707	21709	SNP	1		G/A
18	AC007767	1	127462	F5D14	473723	78421	78423	SNP	1		C/A
18	AC007767	1	127462	F5D14	473724	79599	79601	SNP	1		C/A
18	AC007767	1	127462	F5D14	473725	79597	79599	SNP	1		G/A
18	AC007767	1	127462	F5D14	473726	79488	79490	SNP	1		T/A
18	AC007767	1	127462	F5D14	473727	79126	79128	SNP	1		G/A
18	AC007767	1	127462	F5D14	473728	79122	79124	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
18	AC007767	1	127462	F5D14	473729	79538	79540	SNP	1		T/C
18	AC007767	1	127462	F5D14	473730	79527	79529	SNP	1		G/C
18	AC007767	1	127462	F5D14	473731	79523	79525	SNP	1		T/G
18	AC007767	1	127462	F5D14	473912	1046	1047	IND	2	-3/3	
18	AC007767	1	127462	F5D14	473913	1488	1489	IND	2	-4/4	
18	AC007767	1	127462	F5D14	473914	162	170	IND	2	7/-7	
18	AC007767	1	127462	F5D14	473915	524	525	IND	2	-4/4	
18	AC007767	1	127462	F5D14	474246	104613	104614	IND	1	-2/2	
18	AC007767	1	127462	F5D14	474247	1047	1048	IND	1	-3/3	
18	AC007767	1	127462	F5D14	474248	1490	1491	IND	1	-1/1	
18	AC007767	1	127462	F5D14	474249	1491	1492	IND	1	-3/3	
18	AC007767	1	127462	F5D14	474250	34852	34855	IND	1	2/-2	
18	AC007767	1	127462	F5D14	474251	34856	34858	IND	1	1/-1	
18	AC007767	1	127462	F5D14	474252	34858	34861	IND	1	2/-2	
18	AC007767	1	127462	F5D14	474253	76617	76619	IND	1	1/-1	
18	AC007767	1	127462	F5D14	474254	79600	79601	IND	1	-1/1	
19	AC008046	1	94618	F5A13	466999	76801	76803	SNP	1		A/T
19	AC008046	1	94618	F5A13	467791	78462	78464	SNP	1		G/A
19	AC008046	1	94618	F5A13	469419	69132	69134	SNP	1		T/A
19	AC008046	1	94618	F5A13	469420	69294	69296	SNP	1		C/A
19	AC008046	1	94618	F5A13	469421	69170	69172	SNP	1		C/G
19	AC008046	1	94618	F5A13	470303	50766	50767	IND	2	-8/8	
19	AC008046	1	94618	F5A13	470304	88783	88805	IND	2	21/-21	
19	AC008046	1	94618	F5A13	471343	92630	92632	IND	1	1/-1	
20	AC009526	1	108061	F2J6	470130	101759	101763	IND	2	3/-3	
20	AC009526	1	108061	F2J6	470131	101865	102686	IND	2	820/-820	
20	AC009526	1	108061	F2J6	470132	107351	107352	IND	2	-12/12	
20	AC009526	1	108061	F2J6	470133	107550	107551	IND	2	-9/9	
20	AC009526	1	108061	F2J6	470134	19533	19578	IND	2	44/-44	
20	AC009526	1	108061	F2J6	470135	30524	30525	IND	2	-13/13	
20	AC009526	1	108061	F2J6	470136	30591	30595	IND	2	3/-3	
20	AC009526	1	108061	F2J6	470137	35894	35899	IND	2	4/-4	
20	AC009526	1	108061	F2J6	470138	52991	52992	IND	2	-6/6	
20	AC009526	1	108061	F2J6	470139	56213	56214	IND	2	-4/4	
20	AC009526	1	108061	F2J6	470140	61125	61134	IND	2	8/-8	
20	AC009526	1	108061	F2J6	470141	6195	6201	IND	2	5/-5	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
20	AC009526	1	108061	F2J6	470142	68412	68456	IND	2	43/-43	
20	AC009526	1	108061	F2J6	470143	71322	71329	IND	2	6/-6	
20	AC009526	1	108061	F2J6	470144	72080	72096	IND	2	15/-15	
20	AC009526	1	108061	F2J6	470145	72103	81241	IND	2	9137/-9137	
20	AC009526	1	108061	F2J6	470146	72105	72121	IND	2	15/-15	
20	AC009526	1	108061	F2J6	470147	73956	73969	IND	2	12/-12	
20	AC009526	1	108061	F2J6	470148	7708	7709	IND	2	-4/4	
20	AC009526	1	108061	F2J6	470149	80459	80466	IND	2	6/-6	
20	AC009526	1	108061	F2J6	470150	83084	83097	IND	2	12/-12	
20	AC009526	1	108061	F2J6	470151	91873	91920	IND	2	46/-46	
20	AC009526	1	108061	F2J6	470152	98451	98455	IND	2	3/-3	
21	AC006423	1	131692	F28H19	467834	56238	56240	SNP	1		G/A
21	AC006423	1	131692	F28H19	467835	56359	56361	SNP	1		A/C
21	AC006423	1	131692	F28H19	467836	56246	56248	SNP	1		G/T
21	AC006423	1	131692	F28H19	468042	45985	45987	SNP	1		G/A
21	AC006423	1	131692	F28H19	468838	100537	100539	SNP	1		C/A
21	AC006423	1	131692	F28H19	470073	1185	1256	IND	2	70/-70	
21	AC006423	1	131692	F28H19	470074	118608	118609	IND	2	-86/86	
21	AC006423	1	131692	F28H19	470075	121798	121799	IND	2	-74/74	
21	AC006423	1	131692	F28H19	470076	122811	122815	IND	2	3/-3	
21	AC006423	1	131692	F28H19	470077	16412	16416	IND	2	3/-3	
21	AC006423	1	131692	F28H19	470078	1761	1762	IND	2	-17/17	
21	AC006423	1	131692	F28H19	470079	19720	19724	IND	2	3/-3	
21	AC006423	1	131692	F28H19	470080	19826	20647	IND	2	820/-820	
21	AC006423	1	131692	F28H19	470081	27106	27138	IND	2	31/-31	
21	AC006423	1	131692	F28H19	470082	2762	3579	IND	2	816/-816	
21	AC006423	1	131692	F28H19	470083	39500	39510	IND	2	9/-9	
21	AC006423	1	131692	F28H19	470084	82675	82738	IND	2	62/-62	
21	AC006423	1	131692	F28H19	470085	85178	85179	IND	2	-19/19	
21	AC006423	1	131692	F28H19	470086	9834	9881	IND	2	46/-46	
21	AC006423	1	131692	F28H19	471276	55972	55975	IND	1	2/-2	
22	AC007915	1	137336	F27F5	471640	52758	52760	SNP	1		G/A
22	AC007915	1	137336	F27F5	471641	52862	52864	SNP	1		T/C
22	AC007915	1	137336	F27F5	471642	52970	52972	SNP	1		T/G
22	AC007915	1	137336	F27F5	471643	52777	52779	SNP	1		T/G
22	AC007915	1	137336	F27F5	471644	52742	52744	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
22	AC007915	1	137336	F27F5	471645	52689	52691	SNP	1		C/T
22	AC007915	1	137336	F27F5	471722	51108	51110	SNP	1		G/A
22	AC007915	1	137336	F27F5	471723	50978	50980	SNP	1		T/C
22	AC007915	1	137336	F27F5	471724	51113	51115	SNP	1		A/G
22	AC007915	1	137336	F27F5	471808	123656	123658	SNP	1		A/G
22	AC007915	1	137336	F27F5	471833	122870	122872	SNP	1		T/C
22	AC007915	1	137336	F27F5	472413	111584	111586	SNP	1		G/A
22	AC007915	1	137336	F27F5	472414	111534	111536	SNP	1		A/C
22	AC007915	1	137336	F27F5	472494	84989	84991	SNP	1		G/A
22	AC007915	1	137336	F27F5	472495	85991	85993	SNP	1		T/C
22	AC007915	1	137336	F27F5	472496	84908	84910	SNP	1		T/C
22	AC007915	1	137336	F27F5	472497	85887	85889	SNP	1		A/G
22	AC007915	1	137336	F27F5	472498	84832	84834	SNP	1		A/G
22	AC007915	1	137336	F27F5	472499	85930	85932	SNP	1		C/T
22	AC007915	1	137336	F27F5	472500	85989	85991	SNP	1		G/T
22	AC007915	1	137336	F27F5	472501	85213	85215	SNP	1		C/T
22	AC007915	1	137336	F27F5	472509	81731	81733	SNP	1		G/A
22	AC007915	1	137336	F27F5	472510	79728	79730	SNP	1		T/A
22	AC007915	1	137336	F27F5	472511	81382	81384	SNP	1		G/A
22	AC007915	1	137336	F27F5	472512	81088	81090	SNP	1		C/A
22	AC007915	1	137336	F27F5	472513	79773	79775	SNP	1		T/C
22	AC007915	1	137336	F27F5	472514	81184	81186	SNP	1		T/G
22	AC007915	1	137336	F27F5	472515	80937	80939	SNP	1		C/T
22	AC007915	1	137336	F27F5	472516	77188	77190	SNP	1		C/A
22	AC007915	1	137336	F27F5	472517	76654	76656	SNP	1		C/A
22	AC007915	1	137336	F27F5	472518	76631	76633	SNP	1		A/C
22	AC007915	1	137336	F27F5	472519	77506	77508	SNP	1		A/C
22	AC007915	1	137336	F27F5	472520	77308	77310	SNP	1		A/G
22	AC007915	1	137336	F27F5	472521	76798	76800	SNP	1		A/G
22	AC007915	1	137336	F27F5	472522	76623	76625	SNP	1		G/T
22	AC007915	1	137336	F27F5	472573	107287	107289	SNP	1		G/C
22	AC007915	1	137336	F27F5	472717	105558	105560	SNP	1		A/G
22	AC007915	1	137336	F27F5	472718	102963	102965	SNP	1		G/A
22	AC007915	1	137336	F27F5	472719	102990	102992	SNP	1		G/A
22	AC007915	1	137336	F27F5	472720	103058	103060	SNP	1		G/A
22	AC007915	1	137336	F27F5	472721	102959	102961	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
22	AC007915	1	137336	F27F5	472722	103113	103115	SNP	1		G/C
22	AC007915	1	137336	F27F5	472723	102868	102870	SNP	1		C/T
22	AC007915	1	137336	F27F5	472724	103022	103024	SNP	1		C/T
22	AC007915	1	137336	F27F5	473639	113949	113951	SNP	1		C/T
22	AC007915	1	137336	F27F5	473658	92991	92993	SNP	1		T/G
22	AC007915	1	137336	F27F5	473659	93111	93113	SNP	1		T/G
22	AC007915	1	137336	F27F5	473803	102387	102389	SNP	1		T/G
22	AC007915	1	137336	F27F5	474161	101924	101925	IND	1	-1/1	
22	AC007915	1	137336	F27F5	474162	101937	101938	IND	1	-2/2	
22	AC007915	1	137336	F27F5	474163	102271	102273	IND	1	1/-1	
22	AC007915	1	137336	F27F5	474164	122426	122428	IND	1	1/-1	
22	AC007915	1	137336	F27F5	474165	124140	124148	IND	1	7/-7	
22	AC007915	1	137336	F27F5	474166	89612	89613	IND	1	-1/1	
22	AC007915	1	137336	F27F5	474167	92947	92949	IND	1	1/-1	
23	AC015449	1	77424	T3F24	467028	34756	34758	SNP	1		C/A
23	AC015449	1	77424	T3F24	467029	34632	34634	SNP	1		T/G
23	AC015449	1	77424	T3F24	467030	34997	34999	SNP	1		T/G
23	AC015449	1	77424	T3F24	467655	71805	71807	SNP	1		G/A
23	AC015449	1	77424	T3F24	467898	49215	49217	SNP	1		G/A
23	AC015449	1	77424	T3F24	467899	49068	49070	SNP	1		A/T
23	AC015449	1	77424	T3F24	468214	54636	54638	SNP	1		G/C
23	AC015449	1	77424	T3F24	468215	55428	55430	SNP	1		A/G
23	AC015449	1	77424	T3F24	468411	18019	18021	SNP	1		G/A
23	AC015449	1	77424	T3F24	468486	43187	43189	SNP	1		C/A
23	AC015449	1	77424	T3F24	468487	43023	43025	SNP	1		C/A
23	AC015449	1	77424	T3F24	468488	42907	42909	SNP	1		G/C
23	AC015449	1	77424	T3F24	470956	30806	30823	IND	2	16/-16	
23	AC015449	1	77424	T3F24	470957	30994	30998	IND	2	3/-3	
23	AC015449	1	77424	T3F24	470958	31037	31038	IND	2	-3/3	
23	AC015449	1	77424	T3F24	470959	36749	47227	IND	2	10477/-10477	
23	AC015449	1	77424	T3F24	470960	39303	39304	IND	2	-4/4	
23	AC015449	1	77424	T3F24	470961	39647	39658	IND	2	10/-10	
23	AC015449	1	77424	T3F24	470962	49079	49083	IND	2	3/-3	
23	AC015449	1	77424	T3F24	470963	51287	51307	IND	2	19/-19	
23	AC015449	1	77424	T3F24	470964	5731	5732	IND	2	-13/13	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
23	AC015449	1	77424	T3F24	470965	64773	65066	IND	2	292/-292	
23	AC015449	1	77424	T3F24	470966	66856	66894	IND	2	37/-37	
23	AC015449	1	77424	T3F24	470967	77009	77010	IND	2	-8/8	
23	AC015449	1	77424	T3F24	470968	7750	7754	IND	2	3/-3	
23	AC015449	1	77424	T3F24	470969	7754	7758	IND	2	3/-3	
23	AC015449	1	77424	T3F24	471579	34596	34599	IND	1	2/-2	
23	AC015449	1	77424	T3F24	471580	49097	49100	IND	1	2/-2	
24	AC012463	1	97154	T2E6	467168	50795	50797	SNP	1		A/G
24	AC012463	1	97154	T2E6	467169	50685	50687	SNP	1		C/T
24	AC012463	1	97154	T2E6	467489	15353	15355	SNP	1		C/A
24	AC012463	1	97154	T2E6	467935	75124	75126	SNP	1		G/C
24	AC012463	1	97154	T2E6	467936	75661	75663	SNP	1		C/G
24	AC012463	1	97154	T2E6	468257	84322	84324	SNP	1		T/C
24	AC012463	1	97154	T2E6	468258	84327	84329	SNP	1		A/C
24	AC012463	1	97154	T2E6	468259	84525	84527	SNP	1		T/C
24	AC012463	1	97154	T2E6	468260	84424	84426	SNP	1		A/G
24	AC012463	1	97154	T2E6	468330	1754	1756	SNP	1		G/A
24	AC012463	1	97154	T2E6	468331	1682	1684	SNP	1		T/C
24	AC012463	1	97154	T2E6	468332	1655	1657	SNP	1		A/G
24	AC012463	1	97154	T2E6	468344	9329	9331	SNP	1		C/T
24	AC012463	1	97154	T2E6	469239	200	202	SNP	1		T/A
24	AC012463	1	97154	T2E6	469461	73652	73654	SNP	1		C/A
24	AC012463	1	97154	T2E6	469462	73695	73697	SNP	1		T/C
24	AC012463	1	97154	T2E6	470908	17327	19905	IND	2	2577/-2577	
24	AC012463	1	97154	T2E6	470909	18636	18641	IND	2	4/-4	
24	AC012463	1	97154	T2E6	470910	25115	25126	IND	2	10/-10	
24	AC012463	1	97154	T2E6	470911	35204	35205	IND	2	-9/9	
24	AC012463	1	97154	T2E6	470912	37533	37534	IND	2	-4/4	
24	AC012463	1	97154	T2E6	470913	43730	68815	IND	2	25084/-25084	
24	AC012463	1	97154	T2E6	470914	47564	48161	IND	2	596/-596	
24	AC012463	1	97154	T2E6	470915	71869	71870	IND	2	-15/15	
24	AC012463	1	97154	T2E6	470916	72307	72308	IND	2	-3/3	
24	AC012463	1	97154	T2E6	471561	15400	15403	IND	1	2/-2	
24	AC012463	1	97154	T2E6	471562	47315	47316	IND	1	-1/1	
24	AC012463	1	97154	T2E6	471563	47509	47510	IND	1	-1/1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
24	AC012463	1	97154	T2E6	471564	94139	94140	IND	1	-1/1	
25	AC016041	1	119091	F27J15	466876	111878	111880	SNP	1		C/A
25	AC016041	1	119091	F27J15	466884	73939	73941	SNP	1		A/G
25	AC016041	1	119091	F27J15	467011	76926	76928	SNP	1		C/T
25	AC016041	1	119091	F27J15	467012	76735	76737	SNP	1		A/T
25	AC016041	1	119091	F27J15	467052	87312	87314	SNP	1		A/C
25	AC016041	1	119091	F27J15	467053	87226	87228	SNP	1		T/C
25	AC016041	1	119091	F27J15	467054	87437	87439	SNP	1		A/T
25	AC016041	1	119091	F27J15	467176	18913	18915	SNP	1		A/T
25	AC016041	1	119091	F27J15	467250	113731	113733	SNP	1		G/A
25	AC016041	1	119091	F27J15	467251	113708	113710	SNP	1		G/A
25	AC016041	1	119091	F27J15	467252	113839	113841	SNP	1		G/C
25	AC016041	1	119091	F27J15	467253	113699	113701	SNP	1		C/G
25	AC016041	1	119091	F27J15	467254	113894	113896	SNP	1		G/T
25	AC016041	1	119091	F27J15	467351	13161	13163	SNP	1		G/A
25	AC016041	1	119091	F27J15	467352	12762	12764	SNP	1		G/C
25	AC016041	1	119091	F27J15	467353	12915	12917	SNP	1		T/C
25	AC016041	1	119091	F27J15	467782	47775	47777	SNP	1		C/A
25	AC016041	1	119091	F27J15	468171	68630	68632	SNP	1		T/C
25	AC016041	1	119091	F27J15	468172	68598	68600	SNP	1		C/T
25	AC016041	1	119091	F27J15	468173	67148	67150	SNP	1		C/A
25	AC016041	1	119091	F27J15	468174	66942	66944	SNP	1		T/A
25	AC016041	1	119091	F27J15	468175	66945	66947	SNP	1		C/A
25	AC016041	1	119091	F27J15	468176	66360	66362	SNP	1		G/C
25	AC016041	1	119091	F27J15	468177	66980	66982	SNP	1		A/C
25	AC016041	1	119091	F27J15	468178	66112	66114	SNP	1		A/G
25	AC016041	1	119091	F27J15	468447	39378	39380	SNP	1		C/G
25	AC016041	1	119091	F27J15	468515	36924	36926	SNP	1		G/A
25	AC016041	1	119091	F27J15	468886	100659	100661	SNP	1		C/A
25	AC016041	1	119091	F27J15	468887	100653	100655	SNP	1		T/A
25	AC016041	1	119091	F27J15	468888	100005	100007	SNP	1		T/A
25	AC016041	1	119091	F27J15	468889	99854	99856	SNP	1		T/C
25	AC016041	1	119091	F27J15	468890	100687	100689	SNP	1		G/C
25	AC016041	1	119091	F27J15	468891	100633	100635	SNP	1		C/G
25	AC016041	1	119091	F27J15	468892	100580	100582	SNP	1		A/G
25	AC016041	1	119091	F27J15	468893	100452	100454	SNP	1		A/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
25	AC016041	1	119091	F27J15	468894	100550	100552	SNP	1		C/T
25	AC016041	1	119091	F27J15	468895	100539	100541	SNP	1		A/T
25	AC016041	1	119091	F27J15	468896	100127	100129	SNP	1		C/T
25	AC016041	1	119091	F27J15	468897	101340	101342	SNP	1		A/T
25	AC016041	1	119091	F27J15	469014	85004	85006	SNP	1		T/A
25	AC016041	1	119091	F27J15	469015	85045	85047	SNP	1		T/C
25	AC016041	1	119091	F27J15	469276	7163	7165	SNP	1		G/A
25	AC016041	1	119091	F27J15	469277	7201	7203	SNP	1		T/G
25	AC016041	1	119091	F27J15	469278	7271	7273	SNP	1		T/G
25	AC016041	1	119091	F27J15	469368	118143	118145	SNP	1		G/A
25	AC016041	1	119091	F27J15	469369	118567	118569	SNP	1		C/A
25	AC016041	1	119091	F27J15	469370	115573	115575	SNP	1		C/A
25	AC016041	1	119091	F27J15	469371	117816	117818	SNP	1		C/T
25	AC016041	1	119091	F27J15	469372	115360	115362	SNP	1		C/T
25	AC016041	1	119091	F27J15	470047	100571	100576	IND	2	4/-4	
25	AC016041	1	119091	F27J15	470048	10267	10274	IND	2	6/-6	
25	AC016041	1	119091	F27J15	470049	1204	1209	IND	2	4/-4	
25	AC016041	1	119091	F27J15	470050	14562	14576	IND	2	13/-13	
25	AC016041	1	119091	F27J15	470051	38051	38058	IND	2	6/-6	
25	AC016041	1	119091	F27J15	470052	41840	41841	IND	2	-8/8	
25	AC016041	1	119091	F27J15	470053	41989	41990	IND	2	-36/36	
25	AC016041	1	119091	F27J15	470054	42407	42412	IND	2	4/-4	
25	AC016041	1	119091	F27J15	470055	42412	42417	IND	2	4/-4	
25	AC016041	1	119091	F27J15	470056	47910	47911	IND	2	-3/3	
25	AC016041	1	119091	F27J15	470057	51561	51562	IND	2	-4/4	
25	AC016041	1	119091	F27J15	470058	55710	55711	IND	2	-9/9	
25	AC016041	1	119091	F27J15	470059	56634	56647	IND	2	12/-12	
25	AC016041	1	119091	F27J15	470060	57119	57120	IND	2	-21/21	
25	AC016041	1	119091	F27J15	470061	57124	57125	IND	2	-21/21	
25	AC016041	1	119091	F27J15	470062	58286	58287	IND	2	-5/5	
25	AC016041	1	119091	F27J15	470063	5833	5837	IND	2	3/-3	
25	AC016041	1	119091	F27J15	470064	58886	59093	IND	2	206/-206	
25	AC016041	1	119091	F27J15	470065	59483	59514	IND	2	30/-30	
25	AC016041	1	119091	F27J15	470066	60540	60541	IND	2	-15/15	
25	AC016041	1	119091	F27J15	470067	79670	79671	IND	2	-4/4	
25	AC016041	1	119091	F27J15	470068	81310	81311	IND	2	-12/12	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
25	AC016041	1	119091	F27J15	470069	83553	83562	IND	2	8/-8	
25	AC016041	1	119091	F27J15	470070	89221	89225	IND	2	3/-3	
25	AC016041	1	119091	F27J15	470071	96467	96468	IND	2	-10/10	
25	AC016041	1	119091	F27J15	470072	96785	96811	IND	2	25/-25	
25	AC016041	1	119091	F27J15	471269	100507	100509	IND	1	1/-1	
25	AC016041	1	119091	F27J15	471270	100574	100576	IND	1	1/-1	
25	AC016041	1	119091	F27J15	471271	100578	100580	IND	1	1/-1	
25	AC016041	1	119091	F27J15	471272	100583	100586	IND	1	2/-2	
25	AC016041	1	119091	F27J15	471273	100683	100685	IND	1	1/-1	
25	AC016041	1	119091	F27J15	471274	12773	12774	IND	1	-1/1	
25	AC016041	1	119091	F27J15	471275	28850	28853	IND	1	2/-2	
26	AC011807	1	104679	F14J22	466801	32196	32198	SNP	1		T/A
26	AC011807	1	104679	F14J22	466815	67646	67648	SNP	1		C/G
26	AC011807	1	104679	F14J22	466816	67526	67528	SNP	1		C/T
26	AC011807	1	104679	F14J22	467034	90892	90894	SNP	1		T/C
26	AC011807	1	104679	F14J22	467303	23796	23798	SNP	1		T/C
26	AC011807	1	104679	F14J22	467343	10923	10925	SNP	1		G/A
26	AC011807	1	104679	F14J22	467344	10891	10893	SNP	1		G/A
26	AC011807	1	104679	F14J22	467345	10505	10507	SNP	1		A/G
26	AC011807	1	104679	F14J22	467346	10995	10997	SNP	1		T/G
26	AC011807	1	104679	F14J22	467347	10947	10949	SNP	1		A/G
26	AC011807	1	104679	F14J22	467643	33686	33688	SNP	1		C/A
26	AC011807	1	104679	F14J22	467645	92289	92291	SNP	1		A/G
26	AC011807	1	104679	F14J22	467669	88503	88505	SNP	1		G/A
26	AC011807	1	104679	F14J22	467670	88591	88593	SNP	1		A/G
26	AC011807	1	104679	F14J22	467671	87980	87982	SNP	1		G/T
26	AC011807	1	104679	F14J22	467672	88605	88607	SNP	1		A/T
26	AC011807	1	104679	F14J22	468126	28123	28125	SNP	1		T/C
26	AC011807	1	104679	F14J22	468516	34621	34623	SNP	1		A/G
26	AC011807	1	104679	F14J22	468567	7997	7999	SNP	1		G/C
26	AC011807	1	104679	F14J22	468568	8117	8119	SNP	1		C/T
26	AC011807	1	104679	F14J22	468569	37685	37687	SNP	1		G/A
26	AC011807	1	104679	F14J22	468570	37020	37022	SNP	1		T/A
26	AC011807	1	104679	F14J22	468571	37183	37185	SNP	1		A/G
26	AC011807	1	104679	F14J22	468572	37209	37211	SNP	1		A/T
26	AC011807	1	104679	F14J22	468819	68624	68626	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
26	AC011807	1	104679	F14J22	468820	68200	68202	SNP	1		G/A
26	AC011807	1	104679	F14J22	468821	68366	68368	SNP	1		A/C
26	AC011807	1	104679	F14J22	468822	68240	68242	SNP	1		G/C
26	AC011807	1	104679	F14J22	468823	68759	68761	SNP	1		T/C
26	AC011807	1	104679	F14J22	468968	94149	94151	SNP	1		C/G
26	AC011807	1	104679	F14J22	469610	17796	17797	IND	2	-6/6	
26	AC011807	1	104679	F14J22	469611	17802	17803	IND	2	-6/6	
26	AC011807	1	104679	F14J22	469612	25708	25717	IND	2	8/-8	
26	AC011807	1	104679	F14J22	469613	38382	38394	IND	2	11/-11	
26	AC011807	1	104679	F14J22	469614	50134	50138	IND	2	3/-3	
26	AC011807	1	104679	F14J22	469615	57082	57089	IND	2	6/-6	
26	AC011807	1	104679	F14J22	469616	61151	61152	IND	2	-3/3	
26	AC011807	1	104679	F14J22	469617	61221	61229	IND	2	7/-7	
26	AC011807	1	104679	F14J22	469618	61450	61451	IND	2	-4/4	
26	AC011807	1	104679	F14J22	469619	71919	71923	IND	2	3/-3	
26	AC011807	1	104679	F14J22	469620	72574	72575	IND	2	-8/8	
26	AC011807	1	104679	F14J22	469621	76648	76649	IND	2	-4/4	
26	AC011807	1	104679	F14J22	469622	77214	77215	IND	2	-3/3	
26	AC011807	1	104679	F14J22	469623	77216	77217	IND	2	-3/3	
26	AC011807	1	104679	F14J22	469624	77223	77224	IND	2	-3/3	
26	AC011807	1	104679	F14J22	469625	85374	85375	IND	2	-6/6	
26	AC011807	1	104679	F14J22	469626	86283	86284	IND	2	-6/6	
26	AC011807	1	104679	F14J22	469627	86284	86285	IND	2	-6/6	
26	AC011807	1	104679	F14J22	469628	86287	86288	IND	2	-6/6	
26	AC011807	1	104679	F14J22	469629	86734	86735	IND	2	-15/15	
26	AC011807	1	104679	F14J22	469630	91542	91547	IND	2	4/-4	
26	AC011807	1	104679	F14J22	469631	92194	92199	IND	2	4/-4	
26	AC011807	1	104679	F14J22	469632	94791	94792	IND	2	-6/6	
26	AC011807	1	104679	F14J22	471117	20797	20798	IND	1	-1/1	
26	AC011807	1	104679	F14J22	471118	37241	37242	IND	1	-1/1	
26	AC011807	1	104679	F14J22	471119	7849	7851	IND	1	1/-1	
26	AC011807	1	104679	F14J22	471120	91546	91549	IND	1	2/-2	
27	AC015445	1	91720	F2J10	470119	38856	38865	IND	2	8/-8	
27	AC015445	1	91720	F2J10	470120	61552	61553	IND	2	-6/6	
27	AC015445	1	91720	F2J10	470121	6233	6268	IND	2	34/-34	
27	AC015445	1	91720	F2J10	470122	63555	63560	IND	2	4/-4	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
27	AC015445	1	91720	F2J10	470123	63978	63979	IND	2	-3/3	
27	AC015445	1	91720	F2J10	470124	70634	70638	IND	2	3/-3	
27	AC015445	1	91720	F2J10	470125	78373	78377	IND	2	3/-3	
27	AC015445	1	91720	F2J10	470126	84030	84087	IND	2	56/-56	
27	AC015445	1	91720	F2J10	470127	84159	84168	IND	2	8/-8	
27	AC015445	1	91720	F2J10	470128	85004	85005	IND	2	-4/4	
27	AC015445	1	91720	F2J10	470129	89454	89459	IND	2	4/-4	
28	AC009323	1	141753	F25P12	466882	120687	120689	SNP	1		G/A
28	AC009323	1	141753	F25P12	466883	120985	120987	SNP	1		C/A
28	AC009323	1	141753	F25P12	467143	54743	54745	SNP	1		T/A
28	AC009323	1	141753	F25P12	467691	122378	122380	SNP	1		T/A
28	AC009323	1	141753	F25P12	467802	124788	124790	SNP	1		G/A
28	AC009323	1	141753	F25P12	467803	124897	124899	SNP	1		T/A
28	AC009323	1	141753	F25P12	467804	124784	124786	SNP	1		A/C
28	AC009323	1	141753	F25P12	467805	124908	124910	SNP	1		T/G
28	AC009323	1	141753	F25P12	467806	125050	125052	SNP	1		A/G
28	AC009323	1	141753	F25P12	467807	124744	124746	SNP	1		A/G
28	AC009323	1	141753	F25P12	467808	124803	124805	SNP	1		G/T
28	AC009323	1	141753	F25P12	469079	129003	129005	SNP	1		T/A
28	AC009323	1	141753	F25P12	469408	67029	67031	SNP	1		G/T
28	AC009323	1	141753	F25P12	469412	75158	75160	SNP	1		G/A
28	AC009323	1	141753	F25P12	469413	74646	74648	SNP	1		G/A
28	AC009323	1	141753	F25P12	469414	74206	74208	SNP	1		T/C
28	AC009323	1	141753	F25P12	469415	74600	74602	SNP	1		T/C
28	AC009323	1	141753	F25P12	469416	74059	74061	SNP	1		C/G
28	AC009323	1	141753	F25P12	469417	74583	74585	SNP	1		A/T
28	AC009323	1	141753	F25P12	469444	109433	109435	SNP	1		A/G
28	AC009323	1	141753	F25P12	469445	109386	109388	SNP	1		A/G
28	AC009323	1	141753	F25P12	469446	109235	109237	SNP	1		A/G
28	AC009323	1	141753	F25P12	469447	109262	109264	SNP	1		C/T
28	AC009323	1	141753	F25P12	469448	109260	109262	SNP	1		G/T
28	AC009323	1	141753	F25P12	469984	112133	112164	IND	2	30/-30	
28	AC009323	1	141753	F25P12	469985	113790	113795	IND	2	4/-4	
28	AC009323	1	141753	F25P12	469986	117227	117256	IND	2	28/-28	
28	AC009323	1	141753	F25P12	469987	133520	133525	IND	2	4/-4	
28	AC009323	1	141753	F25P12	469988	133546	133547	IND	2	-4/4	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
28	AC009323	1	141753	F25P12	469989	138260	138261	IND	2	-12/12	
28	AC009323	1	141753	F25P12	469990	140782	140783	IND	2	-9/9	
28	AC009323	1	141753	F25P12	469991	57191	57206	IND	2	14/-14	
28	AC009323	1	141753	F25P12	469992	6686	6700	IND	2	13/-13	
28	AC009323	1	141753	F25P12	469993	67547	67556	IND	2	8/-8	
28	AC009323	1	141753	F25P12	469994	7730	7731	IND	2	-5/5	
28	AC009323	1	141753	F25P12	469995	96664	96672	IND	2	7/-7	
28	AC009323	1	141753	F25P12	469996	96845	96864	IND	2	18/-18	
28	AC009323	1	141753	F25P12	469997	96935	96944	IND	2	8/-8	
28	AC009323	1	141753	F25P12	471242	109270	109272	IND	1	1/-1	
28	AC009323	1	141753	F25P12	471243	124818	124820	IND	1	1/-1	
28	AC009323	1	141753	F25P12	471244	66416	66417	IND	1	-1/1	
28	AC009323	1	141753	F25P12	471245	74587	74588	IND	1	-1/1	
28	AC009323	1	141753	F25P12	471246	74784	74786	IND	1	1/-1	
29	AC008051	1	86014	F19C14	471820	84203	84205	SNP	1		G/A
29	AC008051	1	86014	F19C14	471821	84144	84146	SNP	1		G/A
29	AC008051	1	86014	F19C14	471822	84039	84041	SNP	1		G/A
29	AC008051	1	86014	F19C14	471823	84243	84245	SNP	1		T/G
29	AC008051	1	86014	F19C14	471824	84225	84227	SNP	1		C/T
29	AC008051	1	86014	F19C14	471825	84089	84091	SNP	1		A/T
29	AC008051	1	86014	F19C14	471826	83983	83985	SNP	1		C/T
29	AC008051	1	86014	F19C14	472044	20828	20830	SNP	1		T/G
29	AC008051	1	86014	F19C14	472045	20980	20982	SNP	1		C/T
29	AC008051	1	86014	F19C14	472311	3825	3827	SNP	1		G/A
29	AC008051	1	86014	F19C14	472312	3584	3586	SNP	1		G/T
29	AC008051	1	86014	F19C14	472468	37232	37234	SNP	1		G/C
29	AC008051	1	86014	F19C14	472484	43439	43441	SNP	1		T/A
29	AC008051	1	86014	F19C14	472485	43545	43547	SNP	1		T/C
29	AC008051	1	86014	F19C14	472486	43456	43458	SNP	1		G/T
29	AC008051	1	86014	F19C14	472487	43680	43682	SNP	1		A/T
29	AC008051	1	86014	F19C14	472488	43744	43746	SNP	1		C/T
29	AC008051	1	86014	F19C14	472582	39563	39565	SNP	1		T/A
29	AC008051	1	86014	F19C14	472583	39564	39566	SNP	1		G/A
29	AC008051	1	86014	F19C14	472584	39525	39527	SNP	1		C/T
29	AC008051	1	86014	F19C14	472755	35053	35055	SNP	1		A/C
29	AC008051	1	86014	F19C14	472756	34987	34989	SNP	1		A/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
29	AC008051	1	86014	F19C14	473104	27132	27134	SNP	1		G/A
29	AC008051	1	86014	F19C14	473105	27076	27078	SNP	1		G/C
29	AC008051	1	86014	F19C14	473106	27034	27036	SNP	1		A/G
29	AC008051	1	86014	F19C14	473107	27135	27137	SNP	1		C/T
29	AC008051	1	86014	F19C14	473125	11877	11879	SNP	1		A/T
29	AC008051	1	86014	F19C14	473126	12052	12054	SNP	1		C/T
29	AC008051	1	86014	F19C14	473291	13397	13399	SNP	1		G/A
29	AC008051	1	86014	F19C14	473292	13398	13400	SNP	1		T/C
29	AC008051	1	86014	F19C14	473293	14166	14168	SNP	1		C/T
29	AC008051	1	86014	F19C14	473294	13411	13413	SNP	1		A/T
29	AC008051	1	86014	F19C14	473506	8855	8857	SNP	1		G/A
29	AC008051	1	86014	F19C14	473507	9347	9349	SNP	1		T/C
29	AC008051	1	86014	F19C14	473508	8905	8907	SNP	1		C/T
29	AC008051	1	86014	F19C14	473660	41234	41236	SNP	1		G/C
29	AC008051	1	86014	F19C14	473703	25560	25562	SNP	1		A/T
29	AC008051	1	86014	F19C14	473704	25425	25427	SNP	1		A/T
29	AC008051	1	86014	F19C14	474092	26917	26920	IND	1	2/-2	
29	AC008051	1	86014	F19C14	474093	3554	3556	IND	1	1/-1	
29	AC008051	1	86014	F19C14	474094	43524	43526	IND	1	1/-1	
29	AC008051	1	86014	F19C14	474095	58030	58031	IND	1	-1/1	
30	AC011000	1	98412	F16P17	471683	29770	29772	SNP	1		T/A
30	AC011000	1	98412	F16P17	471684	29809	29811	SNP	1		C/T
30	AC011000	1	98412	F16P17	472067	38051	38053	SNP	1		T/G
30	AC011000	1	98412	F16P17	472245	75478	75480	SNP	1		T/G
30	AC011000	1	98412	F16P17	472363	11639	11641	SNP	1		G/A
30	AC011000	1	98412	F16P17	472364	11282	11284	SNP	1		T/A
30	AC011000	1	98412	F16P17	472365	11522	11524	SNP	1		T/C
30	AC011000	1	98412	F16P17	472366	10841	10843	SNP	1		T/C
30	AC011000	1	98412	F16P17	472367	11171	11173	SNP	1		T/C
30	AC011000	1	98412	F16P17	472368	11540	11542	SNP	1		A/G
30	AC011000	1	98412	F16P17	472369	12925	12927	SNP	1		C/G
30	AC011000	1	98412	F16P17	472370	10726	10728	SNP	1		A/G
30	AC011000	1	98412	F16P17	472371	11609	11611	SNP	1		G/T
30	AC011000	1	98412	F16P17	472529	61515	61517	SNP	1		G/A
30	AC011000	1	98412	F16P17	472530	61330	61332	SNP	1		A/C
30	AC011000	1	98412	F16P17	472531	61159	61161	SNP	1		G/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
30	AC011000	1	98412	F16P17	472532	61727	61729	SNP	1		A/G
30	AC011000	1	98412	F16P17	472533	61700	61702	SNP	1		A/G
30	AC011000	1	98412	F16P17	472534	61256	61258	SNP	1		C/G
30	AC011000	1	98412	F16P17	472916	49026	49028	SNP	1		G/A
30	AC011000	1	98412	F16P17	472917	49502	49504	SNP	1		T/A
30	AC011000	1	98412	F16P17	472918	49510	49512	SNP	1		C/A
30	AC011000	1	98412	F16P17	472919	49665	49667	SNP	1		T/A
30	AC011000	1	98412	F16P17	472920	49020	49022	SNP	1		A/G
30	AC011000	1	98412	F16P17	472921	49320	49322	SNP	1		T/G
30	AC011000	1	98412	F16P17	472922	49752	49754	SNP	1		T/G
30	AC011000	1	98412	F16P17	472945	37469	37471	SNP	1		C/T
30	AC011000	1	98412	F16P17	473116	36159	36161	SNP	1		G/A
30	AC011000	1	98412	F16P17	473158	74647	74649	SNP	1		T/A
30	AC011000	1	98412	F16P17	473159	74440	74442	SNP	1		A/G
30	AC011000	1	98412	F16P17	473160	74437	74439	SNP	1		C/T
30	AC011000	1	98412	F16P17	473204	17997	17999	SNP	1		T/A
30	AC011000	1	98412	F16P17	473205	17932	17934	SNP	1		A/T
30	AC011000	1	98412	F16P17	473206	17974	17976	SNP	1		C/T
30	AC011000	1	98412	F16P17	473755	51640	51642	SNP	1		G/A
30	AC011000	1	98412	F16P17	473756	50682	50684	SNP	1		T/C
30	AC011000	1	98412	F16P17	473757	50375	50377	SNP	1		T/C
30	AC011000	1	98412	F16P17	473758	51701	51703	SNP	1		A/G
30	AC011000	1	98412	F16P17	473759	50354	50356	SNP	1		G/T
30	AC011000	1	98412	F16P17	473760	51560	51562	SNP	1		G/T
30	AC011000	1	98412	F16P17	473797	14198	14200	SNP	1		A/T
30	AC011000	1	98412	F16P17	473842	2593	3110	IND	2	516/-516	
30	AC011000	1	98412	F16P17	473843	3246	3247	IND	2	-5/5	
30	AC011000	1	98412	F16P17	473844	3437	3441	IND	2	3/-3	
30	AC011000	1	98412	F16P17	473845	5953	5962	IND	2	8/-8	
30	AC011000	1	98412	F16P17	474075	12828	12830	IND	1	1/-1	
30	AC011000	1	98412	F16P17	474076	12830	12833	IND	1	2/-2	
30	AC011000	1	98412	F16P17	474077	12833	12837	IND	1	3/-3	
30	AC011000	1	98412	F16P17	474078	12895	12896	IND	1	-1/1	
30	AC011000	1	98412	F16P17	474079	18047	18049	IND	1	1/-1	
30	AC011000	1	98412	F16P17	474080	49295	49296	IND	1	-1/1	
30	AC011000	1	98412	F16P17	474081	49418	49421	IND	1	2/-2	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
30	AC011000	1	98412	F16P17	474082	61244	61245	IND	1	-1/1	
30	AC011000	1	98412	F16P17	474083	61644	61646	IND	1	1/-1	
30	AC011000	1	98412	F16P17	474084	88618	88619	IND	1	-1/1	
30	AC011000	1	98412	F16P17	474085	88812	88813	IND	1	-1/1	
31	AC010795	1	100512	F16M19	467124	31521	31523	SNP	1		G/A
31	AC010795	1	100512	F16M19	467204	50728	50730	SNP	1		T/A
31	AC010795	1	100512	F16M19	467205	50886	50888	SNP	1		T/C
31	AC010795	1	100512	F16M19	467206	49000	49002	SNP	1		A/G
31	AC010795	1	100512	F16M19	467207	48868	48870	SNP	1		T/G
31	AC010795	1	100512	F16M19	467601	57810	57812	SNP	1		T/C
31	AC010795	1	100512	F16M19	467602	56709	56711	SNP	1		T/C
31	AC010795	1	100512	F16M19	467603	57762	57764	SNP	1		T/G
31	AC010795	1	100512	F16M19	467604	56334	56336	SNP	1		A/G
31	AC010795	1	100512	F16M19	469695	32989	32990	IND	2	-3/3	
31	AC010795	1	100512	F16M19	469696	33989	34332	IND	2	342/-342	
31	AC010795	1	100512	F16M19	469697	38266	38275	IND	2	8/-8	
31	AC010795	1	100512	F16M19	469698	65444	65445	IND	2	-3/3	
31	AC010795	1	100512	F16M19	469699	65508	65509	IND	2	-10/10	
31	AC010795	1	100512	F16M19	469700	66562	66563	IND	2	-4/4	
31	AC010795	1	100512	F16M19	469701	66702	66706	IND	2	3/-3	
31	AC010795	1	100512	F16M19	469702	7887	7904	IND	2	16/-16	
31	AC010795	1	100512	F16M19	469703	89548	89549	IND	2	-3/3	
31	AC010795	1	100512	F16M19	469704	9166	9167	IND	2	-3/3	
31	AC010795	1	100512	F16M19	469705	92713	92714	IND	2	-9/9	
31	AC010795	1	100512	F16M19	469706	92715	92716	IND	2	-9/9	
31	AC010795	1	100512	F16M19	471155	49976	49978	IND	1	1/-1	
31	AC010795	1	100512	F16M19	471156	86849	86850	IND	1	-1/1	
31	AC010795	1	100512	F16M19	471157	87045	87046	IND	1	-1/1	
32	AC008047	1	100867	F2K11	467719	47761	47763	SNP	1		G/A
32	AC008047	1	100867	F2K11	467720	48636	48638	SNP	1		C/T
32	AC008047	1	100867	F2K11	467867	37404	37406	SNP	1		G/A
32	AC008047	1	100867	F2K11	467868	37221	37223	SNP	1		T/A
32	AC008047	1	100867	F2K11	468651	57266	57268	SNP	1		T/A
32	AC008047	1	100867	F2K11	468652	56917	56919	SNP	1		T/A
32	AC008047	1	100867	F2K11	468653	57031	57033	SNP	1		T/C
32	AC008047	1	100867	F2K11	468654	57014	57016	SNP	1		G/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
32	AC008047	1	100867	F2K11	468655	57261	57263	SNP	1		C/G
32	AC008047	1	100867	F2K11	468656	56919	56921	SNP	1		C/G
32	AC008047	1	100867	F2K11	468657	57180	57182	SNP	1		C/T
32	AC008047	1	100867	F2K11	468791	53626	53628	SNP	1		T/A
32	AC008047	1	100867	F2K11	468792	53843	53845	SNP	1		A/C
32	AC008047	1	100867	F2K11	468793	53765	53767	SNP	1		A/G
32	AC008047	1	100867	F2K11	468794	53444	53446	SNP	1		T/G
32	AC008047	1	100867	F2K11	468855	94586	94588	SNP	1		T/A
32	AC008047	1	100867	F2K11	468856	95566	95568	SNP	1		T/C
32	AC008047	1	100867	F2K11	468857	94667	94669	SNP	1		A/T
32	AC008047	1	100867	F2K11	468858	96044	96046	SNP	1		A/T
32	AC008047	1	100867	F2K11	468960	20455	20457	SNP	1		G/C
32	AC008047	1	100867	F2K11	468961	20419	20421	SNP	1		G/T
32	AC008047	1	100867	F2K11	468986	64809	64811	SNP	1		T/A
32	AC008047	1	100867	F2K11	468987	64849	64851	SNP	1		A/C
32	AC008047	1	100867	F2K11	468988	63882	63884	SNP	1		C/T
32	AC008047	1	100867	F2K11	469078	50300	50302	SNP	1		G/T
32	AC008047	1	100867	F2K11	469128	18892	18894	SNP	1		C/T
32	AC008047	1	100867	F2K11	469129	15891	15893	SNP	1		A/G
32	AC008047	1	100867	F2K11	469130	25492	25494	SNP	1		T/G
32	AC008047	1	100867	F2K11	469240	73359	73361	SNP	1		G/T
32	AC008047	1	100867	F2K11	469241	70720	70722	SNP	1		C/A
32	AC008047	1	100867	F2K11	469242	70779	70781	SNP	1		C/A
32	AC008047	1	100867	F2K11	469243	69578	69580	SNP	1		G/C
32	AC008047	1	100867	F2K11	469244	69687	69689	SNP	1		A/C
32	AC008047	1	100867	F2K11	469245	69423	69425	SNP	1		A/G
32	AC008047	1	100867	F2K11	470153	12921	12925	IND	2	3/-3	
32	AC008047	1	100867	F2K11	470154	26519	26520	IND	2	-64/64	
32	AC008047	1	100867	F2K11	470155	34635	34636	IND	2	-5/5	
32	AC008047	1	100867	F2K11	470156	348	349	IND	2	-3/3	
32	AC008047	1	100867	F2K11	470157	362	363	IND	2	-11/11	
32	AC008047	1	100867	F2K11	470158	36333	36334	IND	2	-3/3	
32	AC008047	1	100867	F2K11	470159	38271	38272	IND	2	-3/3	
32	AC008047	1	100867	F2K11	470160	40148	40160	IND	2	11/-11	
32	AC008047	1	100867	F2K11	470161	54591	54650	IND	2	58/-58	
32	AC008047	1	100867	F2K11	470162	60065	60069	IND	2	3/-3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
32	AC008047	1	100867	F2K11	470163	69150	69151	IND	2	-60/60	
32	AC008047	1	100867	F2K11	470164	8712	8776	IND	2	63/-63	
32	AC008047	1	100867	F2K11	471297	100610	100612	IND	1	1/-1	
32	AC008047	1	100867	F2K11	471298	48517	48518	IND	1	-1/1	
32	AC008047	1	100867	F2K11	471299	69620	69622	IND	1	1/-1	
32	AC008047	1	100867	F2K11	471300	69898	69899	IND	1	-1/1	
33	AC011020	1	91530	F12B7	467528	84928	84930	SNP	1		G/A
33	AC011020	1	91530	F12B7	468373	86135	86137	SNP	1		C/T
33	AC011020	1	91530	F12B7	469003	74400	74402	SNP	1		T/A
33	AC011020	1	91530	F12B7	469004	74434	74436	SNP	1		T/C
33	AC011020	1	91530	F12B7	469373	72317	72319	SNP	1		C/A
33	AC011020	1	91530	F12B7	469374	71215	71217	SNP	1		G/A
33	AC011020	1	91530	F12B7	469375	71216	71218	SNP	1		G/A
33	AC011020	1	91530	F12B7	469376	71534	71536	SNP	1		G/A
33	AC011020	1	91530	F12B7	469377	72446	72448	SNP	1		T/C
33	AC011020	1	91530	F12B7	469378	71575	71577	SNP	1		G/C
33	AC011020	1	91530	F12B7	469379	71600	71602	SNP	1		G/C
33	AC011020	1	91530	F12B7	469380	73076	73078	SNP	1		A/G
33	AC011020	1	91530	F12B7	469381	71388	71390	SNP	1		A/G
33	AC011020	1	91530	F12B7	469382	71537	71539	SNP	1		A/G
33	AC011020	1	91530	F12B7	469383	71602	71604	SNP	1		C/G
33	AC011020	1	91530	F12B7	469384	71665	71667	SNP	1		A/G
33	AC011020	1	91530	F12B7	469385	71489	71491	SNP	1		C/T
33	AC011020	1	91530	F12B7	469386	71560	71562	SNP	1		G/T
33	AC011020	1	91530	F12B7	469387	71662	71664	SNP	1		A/T
33	AC011020	1	91530	F12B7	469388	71674	71676	SNP	1		C/T
33	AC011020	1	91530	F12B7	469562	2832	2833	IND	2	-4/4	
33	AC011020	1	91530	F12B7	469563	30696	30697	IND	2	-4/4	
33	AC011020	1	91530	F12B7	469564	37378	37385	IND	2	6/-6	
33	AC011020	1	91530	F12B7	469565	41827	41834	IND	2	6/-6	
33	AC011020	1	91530	F12B7	469566	45490	45499	IND	2	8/-8	
33	AC011020	1	91530	F12B7	469567	49474	49480	IND	2	5/-5	
33	AC011020	1	91530	F12B7	469568	49539	49540	IND	2	-5/5	
33	AC011020	1	91530	F12B7	469569	50980	50990	IND	2	9/-9	
33	AC011020	1	91530	F12B7	469570	69480	69489	IND	2	8/-8	
33	AC011020	1	91530	F12B7	469571	69526	69535	IND	2	8/-8	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
33	AC011020	1	91530	F12B7	469572	70013	70017	IND	2	3/-3	
33	AC011020	1	91530	F12B7	469573	70028	70032	IND	2	3/-3	
33	AC011020	1	91530	F12B7	469574	70040	70041	IND	2	-9/9	
33	AC011020	1	91530	F12B7	469575	70139	70140	IND	2	-6/6	
33	AC011020	1	91530	F12B7	469576	70919	70927	IND	2	7/-7	
33	AC011020	1	91530	F12B7	469577	71124	71130	IND	2	5/-5	
33	AC011020	1	91530	F12B7	469578	71143	71147	IND	2	3/-3	
33	AC011020	1	91530	F12B7	469579	75864	75873	IND	2	8/-8	
33	AC011020	1	91530	F12B7	469580	81920	81921	IND	2	-6/6	
33	AC011020	1	91530	F12B7	469581	85193	85194	IND	2	-62/62	
33	AC011020	1	91530	F12B7	471096	72308	72310	IND	1	1/-1	
33	AC011020	1	91530	F12B7	471097	74328	74330	IND	1	1/-1	
33	AC011020	1	91530	F12B7	471098	74483	74484	IND	1	-1/1	
34	AC012654	1	98471	F14O23	466879	86416	86418	SNP	1		C/T
34	AC012654	1	98471	F14O23	467002	97657	97659	SNP	1		C/A
34	AC012654	1	98471	F14O23	467295	63741	63743	SNP	1		T/G
34	AC012654	1	98471	F14O23	467312	7653	7655	SNP	1		T/C
34	AC012654	1	98471	F14O23	467313	8484	8486	SNP	1		A/T
34	AC012654	1	98471	F14O23	467549	44319	44321	SNP	1		A/T
34	AC012654	1	98471	F14O23	467730	28251	28253	SNP	1		G/A
34	AC012654	1	98471	F14O23	467731	28205	28207	SNP	1		T/A
34	AC012654	1	98471	F14O23	467852	84003	84005	SNP	1		C/T
34	AC012654	1	98471	F14O23	468014	76305	76307	SNP	1		A/C
34	AC012654	1	98471	F14O23	468022	94576	94578	SNP	1		C/T
34	AC012654	1	98471	F14O23	468023	94757	94759	SNP	1		A/T
34	AC012654	1	98471	F14O23	468024	94872	94874	SNP	1		C/T
34	AC012654	1	98471	F14O23	468040	24125	24127	SNP	1		T/A
34	AC012654	1	98471	F14O23	468041	24931	24933	SNP	1		A/T
34	AC012654	1	98471	F14O23	468070	48609	48611	SNP	1		C/T
34	AC012654	1	98471	F14O23	468361	47820	47822	SNP	1		G/C
34	AC012654	1	98471	F14O23	468362	47957	47959	SNP	1		T/C
34	AC012654	1	98471	F14O23	468434	96135	96137	SNP	1		C/T
34	AC012654	1	98471	F14O23	468435	96392	96394	SNP	1		A/T
34	AC012654	1	98471	F14O23	468445	60021	60023	SNP	1		G/T
34	AC012654	1	98471	F14O23	468454	35443	35445	SNP	1		T/A
34	AC012654	1	98471	F14O23	468455	35391	35393	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
34	AC012654	1	98471	F14O23	468456	35267	35269	SNP	1		C/A
34	AC012654	1	98471	F14O23	468457	35250	35252	SNP	1		G/A
34	AC012654	1	98471	F14O23	468458	35970	35972	SNP	1		T/G
34	AC012654	1	98471	F14O23	468459	35882	35884	SNP	1		A/G
34	AC012654	1	98471	F14O23	468460	35914	35916	SNP	1		A/T
34	AC012654	1	98471	F14O23	468962	9819	9821	SNP	1		A/T
34	AC012654	1	98471	F14O23	469089	69875	69877	SNP	1		C/T
34	AC012654	1	98471	F14O23	469119	62035	62037	SNP	1		T/A
34	AC012654	1	98471	F14O23	469120	62481	62483	SNP	1		A/C
34	AC012654	1	98471	F14O23	469121	62210	62212	SNP	1		T/G
34	AC012654	1	98471	F14O23	469648	12484	12485	IND	2	-5/5	
34	AC012654	1	98471	F14O23	469649	22310	22321	IND	2	10/-10	
34	AC012654	1	98471	F14O23	469650	22363	22364	IND	2	-6/6	
34	AC012654	1	98471	F14O23	469651	22364	22365	IND	2	-6/6	
34	AC012654	1	98471	F14O23	469652	335	340	IND	2	4/-4	
34	AC012654	1	98471	F14O23	469653	37037	37045	IND	2	7/-7	
34	AC012654	1	98471	F14O23	469654	52879	52883	IND	2	3/-3	
34	AC012654	1	98471	F14O23	469655	77533	77537	IND	2	3/-3	
34	AC012654	1	98471	F14O23	469656	81302	81303	IND	2	-7/7	
34	AC012654	1	98471	F14O23	469657	88902	88903	IND	2	-40/40	
34	AC012654	1	98471	F14O23	471136	24677	24679	IND	1	1/-1	
34	AC012654	1	98471	F14O23	471137	34940	34941	IND	1	-1/1	
34	AC012654	1	98471	F14O23	471138	35943	35945	IND	1	1/-1	
34	AC012654	1	98471	F14O23	471139	35971	35973	IND	1	1/-1	
34	AC012654	1	98471	F14O23	471140	36238	36240	IND	1	1/-1	
34	AC012654	1	98471	F14O23	471141	37043	37045	IND	1	1/-1	
34	AC012654	1	98471	F14O23	471142	37050	37057	IND	1	6/-6	
34	AC012654	1	98471	F14O23	471143	37166	37167	IND	1	-1/1	
34	AC012654	1	98471	F14O23	471144	83762	83764	IND	1	1/-1	
34	AC012654	1	98471	F14O23	471145	86384	86385	IND	1	-1/1	
34	AC012654	1	98471	F14O23	471146	96088	96090	IND	1	1/-1	
35	AC012679	1	105937	F25P22	466850	20970	20972	SNP	1		T/C
35	AC012679	1	105937	F25P22	467077	64106	64108	SNP	1		T/A
35	AC012679	1	105937	F25P22	467078	65648	65650	SNP	1		T/A
35	AC012679	1	105937	F25P22	467079	65608	65610	SNP	1		G/A
35	AC012679	1	105937	F25P22	467080	65470	65472	SNP	1		G/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
35	AC012679	1	105937	F25P22	467081	65243	65245	SNP	1		T/G
35	AC012679	1	105937	F25P22	467082	65654	65656	SNP	1		C/T
35	AC012679	1	105937	F25P22	467338	27554	27556	SNP	1		A/G
35	AC012679	1	105937	F25P22	467418	102780	102782	SNP	1		A/T
35	AC012679	1	105937	F25P22	467721	71234	71236	SNP	1		C/T
35	AC012679	1	105937	F25P22	467776	19880	19882	SNP	1		G/A
35	AC012679	1	105937	F25P22	467777	18547	18549	SNP	1		T/C
35	AC012679	1	105937	F25P22	467883	78541	78543	SNP	1		T/A
35	AC012679	1	105937	F25P22	467884	78596	78598	SNP	1		A/T
35	AC012679	1	105937	F25P22	467885	78545	78547	SNP	1		A/T
35	AC012679	1	105937	F25P22	468031	31151	31153	SNP	1		G/A
35	AC012679	1	105937	F25P22	468032	31114	31116	SNP	1		T/A
35	AC012679	1	105937	F25P22	468033	31077	31079	SNP	1		T/C
35	AC012679	1	105937	F25P22	468034	30954	30956	SNP	1		C/G
35	AC012679	1	105937	F25P22	468369	13932	13934	SNP	1		T/C
35	AC012679	1	105937	F25P22	468370	13934	13936	SNP	1		C/T
35	AC012679	1	105937	F25P22	468380	58103	58105	SNP	1		G/T
35	AC012679	1	105937	F25P22	468622	63573	63575	SNP	1		G/C
35	AC012679	1	105937	F25P22	468623	63582	63584	SNP	1		T/C
35	AC012679	1	105937	F25P22	468624	62876	62878	SNP	1		T/C
35	AC012679	1	105937	F25P22	468625	63561	63563	SNP	1		A/G
35	AC012679	1	105937	F25P22	468626	63585	63587	SNP	1		A/G
35	AC012679	1	105937	F25P22	468627	63588	63590	SNP	1		A/G
35	AC012679	1	105937	F25P22	468628	63591	63593	SNP	1		T/G
35	AC012679	1	105937	F25P22	468629	63607	63609	SNP	1		T/G
35	AC012679	1	105937	F25P22	468630	63083	63085	SNP	1		C/T
35	AC012679	1	105937	F25P22	468631	63536	63538	SNP	1		A/T
35	AC012679	1	105937	F25P22	468632	63551	63553	SNP	1		G/T
35	AC012679	1	105937	F25P22	468633	63560	63562	SNP	1		A/T
35	AC012679	1	105937	F25P22	468634	62822	62824	SNP	1		C/T
35	AC012679	1	105937	F25P22	468635	62828	62830	SNP	1		C/T
35	AC012679	1	105937	F25P22	468636	62852	62854	SNP	1		C/T
35	AC012679	1	105937	F25P22	468639	52558	52560	SNP	1		T/C
35	AC012679	1	105937	F25P22	468640	53368	53370	SNP	1		T/C
35	AC012679	1	105937	F25P22	469254	99551	99553	SNP	1		G/A
35	AC012679	1	105937	F25P22	469255	99632	99634	SNP	1		C/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
35	AC012679	1	105937	F25P22	469354	74000	74002	SNP	1		T/G
35	AC012679	1	105937	F25P22	469998	11134	11135	IND	2	-9/9	
35	AC012679	1	105937	F25P22	469999	26262	26268	IND	2	5/-5	
35	AC012679	1	105937	F25P22	470000	26469	26470	IND	2	-4/4	
35	AC012679	1	105937	F25P22	470001	28232	28236	IND	2	3/-3	
35	AC012679	1	105937	F25P22	470002	2965	2979	IND	2	13/-13	
35	AC012679	1	105937	F25P22	470003	31314	31322	IND	2	7/-7	
35	AC012679	1	105937	F25P22	470004	35106	35124	IND	2	17/-17	
35	AC012679	1	105937	F25P22	470005	35189	35194	IND	2	4/-4	
35	AC012679	1	105937	F25P22	470006	36343	36344	IND	2	-6/6	
35	AC012679	1	105937	F25P22	470007	3815	3830	IND	2	14/-14	
35	AC012679	1	105937	F25P22	470008	3975	3986	IND	2	10/-10	
35	AC012679	1	105937	F25P22	470009	86726	86730	IND	2	3/-3	
35	AC012679	1	105937	F25P22	471247	52250	52252	IND	1	1/-1	
35	AC012679	1	105937	F25P22	471248	56215	56217	IND	1	1/-1	
35	AC012679	1	105937	F25P22	471249	56222	56224	IND	1	1/-1	
35	AC012679	1	105937	F25P22	471250	57505	57506	IND	1	-2/2	
35	AC012679	1	105937	F25P22	471251	61332	61334	IND	1	1/-1	
35	AC012679	1	105937	F25P22	471252	63605	63607	IND	1	1/-1	
35	AC012679	1	105937	F25P22	471253	65584	65585	IND	1	-1/1	
35	AC012679	1	105937	F25P22	471254	65585	65586	IND	1	-1/1	
35	AC012679	1	105937	F25P22	471255	65645	65646	IND	1	-2/2	
35	AC012679	1	105937	F25P22	471256	70985	70986	IND	1	-1/1	
36	AC023754	1	100685	F1B16	472068	75426	75428	SNP	1		T/A
36	AC023754	1	100685	F1B16	472221	88207	88209	SNP	1		A/C
36	AC023754	1	100685	F1B16	472222	86761	86763	SNP	1		G/C
36	AC023754	1	100685	F1B16	472223	88848	88850	SNP	1		T/G
36	AC023754	1	100685	F1B16	472276	9607	9609	SNP	1		C/A
36	AC023754	1	100685	F1B16	472932	15179	15181	SNP	1		T/A
36	AC023754	1	100685	F1B16	473043	92579	92581	SNP	1		T/A
36	AC023754	1	100685	F1B16	473044	93847	93849	SNP	1		T/A
36	AC023754	1	100685	F1B16	473118	90810	90812	SNP	1		T/A
36	AC023754	1	100685	F1B16	473119	90988	90990	SNP	1		T/C
36	AC023754	1	100685	F1B16	473120	91007	91009	SNP	1		C/T
36	AC023754	1	100685	F1B16	473153	60674	60676	SNP	1		G/T
36	AC023754	1	100685	F1B16	473485	38947	38949	SNP	1		A/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
36	AC023754	1	100685	F1B16	473492	36318	36320	SNP	1		G/A
36	AC023754	1	100685	F1B16	473808	10724	10726	SNP	1		C/A
36	AC023754	1	100685	F1B16	473809	10444	10446	SNP	1		C/A
36	AC023754	1	100685	F1B16	473810	10790	10792	SNP	1		T/G
36	AC023754	1	100685	F1B16	473847	21508	21509	IND	2	-6/6	
36	AC023754	1	100685	F1B16	473848	355	381	IND	2	25/-25	
36	AC023754	1	100685	F1B16	473849	5585	5590	IND	2	4/-4	
36	AC023754	1	100685	F1B16	473850	8378	8379	IND	2	-6/6	
36	AC023754	1	100685	F1B16	474096	10449	10450	IND	1	-1/1	
36	AC023754	1	100685	F1B16	474097	13169	13171	IND	1	1/-1	
36	AC023754	1	100685	F1B16	474098	23713	23714	IND	1	-1/1	
36	AC023754	1	100685	F1B16	474099	77983	77984	IND	1	-3/3	
36	AC023754	1	100685	F1B16	474100	8257	8258	IND	1	-1/1	
36	AC023754	1	100685	F1B16	474101	8377	8378	IND	1	-6/6	
36	AC023754	1	100685	F1B16	474102	88853	88856	IND	1	2/-2	
37	AC009978	1	97554	T23E18	466926	25601	25603	SNP	1		T/C
37	AC009978	1	97554	T23E18	466927	25065	25067	SNP	1		C/T
37	AC009978	1	97554	T23E18	466928	25303	25305	SNP	1		C/T
37	AC009978	1	97554	T23E18	467348	47640	47642	SNP	1		A/T
37	AC009978	1	97554	T23E18	467569	6046	6048	SNP	1		T/A
37	AC009978	1	97554	T23E18	467570	5883	5885	SNP	1		C/G
37	AC009978	1	97554	T23E18	467571	6513	6515	SNP	1		C/G
37	AC009978	1	97554	T23E18	467572	6297	6299	SNP	1		A/G
37	AC009978	1	97554	T23E18	467790	46194	46196	SNP	1		G/A
37	AC009978	1	97554	T23E18	468499	33680	33682	SNP	1		G/A
37	AC009978	1	97554	T23E18	468500	33416	33418	SNP	1		C/A
37	AC009978	1	97554	T23E18	468501	37039	37041	SNP	1		T/C
37	AC009978	1	97554	T23E18	468502	34859	34861	SNP	1		A/C
37	AC009978	1	97554	T23E18	468503	32929	32931	SNP	1		G/C
37	AC009978	1	97554	T23E18	468504	32719	32721	SNP	1		G/C
37	AC009978	1	97554	T23E18	468505	37081	37083	SNP	1		T/G
37	AC009978	1	97554	T23E18	468506	32696	32698	SNP	1		A/G
37	AC009978	1	97554	T23E18	468507	34809	34811	SNP	1		G/T
37	AC009978	1	97554	T23E18	468508	33519	33521	SNP	1		A/T
37	AC009978	1	97554	T23E18	468509	33518	33520	SNP	1		A/T
37	AC009978	1	97554	T23E18	468601	45176	45178	SNP	1		C/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
37	AC009978	1	97554	T23E18	468602	45239	45241	SNP	1		T/C
37	AC009978	1	97554	T23E18	468603	45221	45223	SNP	1		A/G
37	AC009978	1	97554	T23E18	468902	30187	30189	SNP	1		T/A
37	AC009978	1	97554	T23E18	468989	43532	43534	SNP	1		A/G
37	AC009978	1	97554	T23E18	469291	10807	10809	SNP	1		T/A
37	AC009978	1	97554	T23E18	469292	11503	11505	SNP	1		T/C
37	AC009978	1	97554	T23E18	469293	12569	12571	SNP	1		A/C
37	AC009978	1	97554	T23E18	469294	12390	12392	SNP	1		T/G
37	AC009978	1	97554	T23E18	469295	11939	11941	SNP	1		G/T
37	AC009978	1	97554	T23E18	469296	10803	10805	SNP	1		G/T
37	AC009978	1	97554	T23E18	469297	12329	12331	SNP	1		C/T
37	AC009978	1	97554	T23E18	469434	13648	13650	SNP	1		T/A
37	AC009978	1	97554	T23E18	469435	14393	14395	SNP	1		T/A
37	AC009978	1	97554	T23E18	470835	1077	1078	IND	2	-26/26	
37	AC009978	1	97554	T23E18	470836	17098	17122	IND	2	23/-23	
37	AC009978	1	97554	T23E18	470837	1862	1874	IND	2	11/-11	
37	AC009978	1	97554	T23E18	470838	1889	1890	IND	2	-13/13	
37	AC009978	1	97554	T23E18	470839	27037	27073	IND	2	35/-35	
37	AC009978	1	97554	T23E18	470840	37245	37250	IND	2	4/-4	
37	AC009978	1	97554	T23E18	470841	45947	45957	IND	2	9/-9	
37	AC009978	1	97554	T23E18	470842	46149	46150	IND	2	-5/5	
37	AC009978	1	97554	T23E18	470843	60406	60407	IND	2	-11/11	
37	AC009978	1	97554	T23E18	470844	60486	60521	IND	2	34/-34	
37	AC009978	1	97554	T23E18	470845	60864	60878	IND	2	13/-13	
37	AC009978	1	97554	T23E18	470846	60899	60904	IND	2	4/-4	
37	AC009978	1	97554	T23E18	470847	63572	63580	IND	2	7/-7	
37	AC009978	1	97554	T23E18	470848	63672	63683	IND	2	10/-10	
37	AC009978	1	97554	T23E18	470849	63748	63753	IND	2	4/-4	
37	AC009978	1	97554	T23E18	470850	64463	64493	IND	2	29/-29	
37	AC009978	1	97554	T23E18	470851	79580	79581	IND	2	-4/4	
37	AC009978	1	97554	T23E18	471536	13695	13696	IND	1	-1/1	
37	AC009978	1	97554	T23E18	471537	44584	44585	IND	1	-2/2	
37	AC009978	1	97554	T23E18	471538	44771	44773	IND	1	1/-1	
37	AC009978	1	97554	T23E18	471539	46150	46151	IND	1	-5/5	
38	AC010704	1	103353	T5M16	466896	38435	38437	SNP	1		G/T
38	AC010704	1	103353	T5M16	467075	11744	11746	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
38	AC010704	1	103353	T5M16	467587	66283	66285	SNP	1		G/A
38	AC010704	1	103353	T5M16	467588	68560	68562	SNP	1		T/C
38	AC010704	1	103353	T5M16	467589	66801	66803	SNP	1		T/C
38	AC010704	1	103353	T5M16	467590	67598	67600	SNP	1		A/T
38	AC010704	1	103353	T5M16	467591	66360	66362	SNP	1		C/T
38	AC010704	1	103353	T5M16	467592	66362	66364	SNP	1		C/T
38	AC010704	1	103353	T5M16	467593	69091	69093	SNP	1		A/T
38	AC010704	1	103353	T5M16	467621	34204	34206	SNP	1		T/A
38	AC010704	1	103353	T5M16	467622	33195	33197	SNP	1		T/C
38	AC010704	1	103353	T5M16	467623	30362	30364	SNP	1		T/A
38	AC010704	1	103353	T5M16	467624	31360	31362	SNP	1		G/C
38	AC010704	1	103353	T5M16	467625	30030	30032	SNP	1		G/C
38	AC010704	1	103353	T5M16	467626	30031	30033	SNP	1		T/C
38	AC010704	1	103353	T5M16	467629	55196	55198	SNP	1		G/A
38	AC010704	1	103353	T5M16	467630	56524	56526	SNP	1		A/G
38	AC010704	1	103353	T5M16	467680	102180	102182	SNP	1		A/G
38	AC010704	1	103353	T5M16	467726	3984	3986	SNP	1		G/A
38	AC010704	1	103353	T5M16	467727	4224	4226	SNP	1		T/C
38	AC010704	1	103353	T5M16	467736	91040	91042	SNP	1		T/G
38	AC010704	1	103353	T5M16	467781	8983	8985	SNP	1		A/C
38	AC010704	1	103353	T5M16	467906	27113	27115	SNP	1		C/G
38	AC010704	1	103353	T5M16	467939	96262	96264	SNP	1		A/T
38	AC010704	1	103353	T5M16	467940	95576	95578	SNP	1		G/T
38	AC010704	1	103353	T5M16	467978	27954	27956	SNP	1		C/T
38	AC010704	1	103353	T5M16	467997	83255	83257	SNP	1		G/C
38	AC010704	1	103353	T5M16	467998	83576	83578	SNP	1		T/C
38	AC010704	1	103353	T5M16	467999	83426	83428	SNP	1		G/T
38	AC010704	1	103353	T5M16	468000	83058	83060	SNP	1		A/T
38	AC010704	1	103353	T5M16	468001	82859	82861	SNP	1		T/C
38	AC010704	1	103353	T5M16	468002	82247	82249	SNP	1		A/C
38	AC010704	1	103353	T5M16	468003	82120	82122	SNP	1		A/T
38	AC010704	1	103353	T5M16	468093	43074	43076	SNP	1		A/G
38	AC010704	1	103353	T5M16	468094	17794	17796	SNP	1		G/C
38	AC010704	1	103353	T5M16	468095	21923	21925	SNP	1		T/C
38	AC010704	1	103353	T5M16	468096	21684	21686	SNP	1		T/G
38	AC010704	1	103353	T5M16	468097	18083	18085	SNP	1		G/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
38	AC010704	1	103353	T5M16	468098	18411	18413	SNP	1		A/T
38	AC010704	1	103353	T5M16	468184	87458	87460	SNP	1		T/C
38	AC010704	1	103353	T5M16	468185	89991	89993	SNP	1		G/A
38	AC010704	1	103353	T5M16	468186	89105	89107	SNP	1		G/C
38	AC010704	1	103353	T5M16	468187	90278	90280	SNP	1		T/C
38	AC010704	1	103353	T5M16	468188	90028	90030	SNP	1		T/C
38	AC010704	1	103353	T5M16	468189	90035	90037	SNP	1		A/G
38	AC010704	1	103353	T5M16	468190	88831	88833	SNP	1		A/T
38	AC010704	1	103353	T5M16	468191	88505	88507	SNP	1		A/T
38	AC010704	1	103353	T5M16	468192	88504	88506	SNP	1		A/T
38	AC010704	1	103353	T5M16	468293	63083	63085	SNP	1		A/C
38	AC010704	1	103353	T5M16	468474	79830	79832	SNP	1		T/A
38	AC010704	1	103353	T5M16	468475	79829	79831	SNP	1		T/C
38	AC010704	1	103353	T5M16	468476	77338	77340	SNP	1		T/C
38	AC010704	1	103353	T5M16	468477	77581	77583	SNP	1		A/G
38	AC010704	1	103353	T5M16	468478	76574	76576	SNP	1		T/G
38	AC010704	1	103353	T5M16	468479	78882	78884	SNP	1		C/G
38	AC010704	1	103353	T5M16	468658	85874	85876	SNP	1		C/A
38	AC010704	1	103353	T5M16	468659	85661	85663	SNP	1		G/A
38	AC010704	1	103353	T5M16	468660	84444	84446	SNP	1		T/C
38	AC010704	1	103353	T5M16	468661	84590	84592	SNP	1		C/T
38	AC010704	1	103353	T5M16	468724	35169	35171	SNP	1		A/T
38	AC010704	1	103353	T5M16	468725	35229	35231	SNP	1		C/T
38	AC010704	1	103353	T5M16	468770	49338	49340	SNP	1		A/T
38	AC010704	1	103353	T5M16	468771	50701	50703	SNP	1		T/A
38	AC010704	1	103353	T5M16	468772	51170	51172	SNP	1		G/A
38	AC010704	1	103353	T5M16	468773	50589	50591	SNP	1		G/C
38	AC010704	1	103353	T5M16	468774	50944	50946	SNP	1		G/C
38	AC010704	1	103353	T5M16	468775	50607	50609	SNP	1		A/G
38	AC010704	1	103353	T5M16	468776	51100	51102	SNP	1		A/G
38	AC010704	1	103353	T5M16	468777	51101	51103	SNP	1		G/T
38	AC010704	1	103353	T5M16	468901	60580	60582	SNP	1		A/C
38	AC010704	1	103353	T5M16	469316	41570	41572	SNP	1		T/A
38	AC010704	1	103353	T5M16	470980	102028	102037	IND	2	8/-8	
38	AC010704	1	103353	T5M16	470981	11820	11827	IND	2	6/-6	
38	AC010704	1	103353	T5M16	470982	13931	13932	IND	2	-3/3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
38	AC010704	1	103353	T5M16	470983	14121	14122	IND	2	-4/4	
38	AC010704	1	103353	T5M16	470984	25172	25173	IND	2	-7/7	
38	AC010704	1	103353	T5M16	470985	44304	44320	IND	2	15/-15	
38	AC010704	1	103353	T5M16	470986	45657	45773	IND	2	115/-115	
38	AC010704	1	103353	T5M16	470987	52947	52948	IND	2	-3/3	
38	AC010704	1	103353	T5M16	470988	53051	53052	IND	2	-3/3	
38	AC010704	1	103353	T5M16	470989	58437	58441	IND	2	3/-3	
38	AC010704	1	103353	T5M16	470990	58447	58451	IND	2	3/-3	
38	AC010704	1	103353	T5M16	470991	78905	78906	IND	2	-3/3	
38	AC010704	1	103353	T5M16	470992	85670	85671	IND	2	-6/6	
38	AC010704	1	103353	T5M16	470993	99425	99435	IND	2	9/-9	
38	AC010704	1	103353	T5M16	471585	102036	102041	IND	1	4/-4	
38	AC010704	1	103353	T5M16	471586	102040	102043	IND	1	2/-2	
38	AC010704	1	103353	T5M16	471587	102044	102046	IND	1	1/-1	
38	AC010704	1	103353	T5M16	471588	2158	2159	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471589	33939	33940	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471590	3878	3879	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471591	41664	41666	IND	1	1/-1	
38	AC010704	1	103353	T5M16	471592	78907	78908	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471593	78908	78909	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471594	85689	85690	IND	1	-6/6	
38	AC010704	1	103353	T5M16	471595	88500	88501	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471596	88501	88502	IND	1	-1/1	
38	AC010704	1	103353	T5M16	471597	96501	96502	IND	1	-1/1	
39	AC013430	1	95771	F3F9	467208	72028	72030	SNP	1		C/A
39	AC013430	1	95771	F3F9	467716	32906	32908	SNP	1		A/G
39	AC013430	1	95771	F3F9	467717	32764	32766	SNP	1		A/T
39	AC013430	1	95771	F3F9	467986	85673	85675	SNP	1		G/A
39	AC013430	1	95771	F3F9	468228	74719	74721	SNP	1		C/T
39	AC013430	1	95771	F3F9	468446	15188	15190	SNP	1		T/A
39	AC013430	1	95771	F3F9	468584	41500	41502	SNP	1		G/A
39	AC013430	1	95771	F3F9	468769	35481	35483	SNP	1		C/T
39	AC013430	1	95771	F3F9	468882	19906	19908	SNP	1		A/G
39	AC013430	1	95771	F3F9	469471	28266	28268	SNP	1		C/A
39	AC013430	1	95771	F3F9	469472	28265	28267	SNP	1		C/A
39	AC013430	1	95771	F3F9	469473	29261	29263	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
39	AC013430	1	95771	F3F9	469474	28809	28811	SNP	1		A/G
39	AC013430	1	95771	F3F9	469475	28271	28273	SNP	1		A/T
39	AC013430	1	95771	F3F9	470236	10166	10189	IND	2	22/-22	
39	AC013430	1	95771	F3F9	470237	15375	15376	IND	2	-4/4	
39	AC013430	1	95771	F3F9	470238	21167	21175	IND	2	7/-7	
39	AC013430	1	95771	F3F9	470239	21874	21883	IND	2	8/-8	
39	AC013430	1	95771	F3F9	470240	23781	23789	IND	2	7/-7	
39	AC013430	1	95771	F3F9	470241	23823	23824	IND	2	-4/4	
39	AC013430	1	95771	F3F9	470242	3254	3255	IND	2	-4/4	
39	AC013430	1	95771	F3F9	470243	38264	38300	IND	2	35/-35	
39	AC013430	1	95771	F3F9	470244	48391	48455	IND	2	63/-63	
39	AC013430	1	95771	F3F9	470245	5953	5962	IND	2	8/-8	
39	AC013430	1	95771	F3F9	470246	62180	62181	IND	2	-3/3	
39	AC013430	1	95771	F3F9	470247	6701	6705	IND	2	3/-3	
39	AC013430	1	95771	F3F9	470248	73998	74005	IND	2	6/-6	
39	AC013430	1	95771	F3F9	470249	74184	74197	IND	2	12/-12	
39	AC013430	1	95771	F3F9	470250	80169	80170	IND	2	-4/4	
39	AC013430	1	95771	F3F9	470251	80685	80693	IND	2	7/-7	
39	AC013430	1	95771	F3F9	470252	8181	8182	IND	2	-3/3	
39	AC013430	1	95771	F3F9	470253	8182	8183	IND	2	-3/3	
39	AC013430	1	95771	F3F9	471316	17004	17005	IND	1	-1/1	
39	AC013430	1	95771	F3F9	471317	29337	29338	IND	1	-1/1	
39	AC013430	1	95771	F3F9	471318	32738	32741	IND	1	2/-2	
40	AC010793	1	90149	F20B17	467129	4800	4802	SNP	1		C/T
40	AC010793	1	90149	F20B17	467130	4205	4207	SNP	1		A/G
40	AC010793	1	90149	F20B17	467984	24874	24876	SNP	1		A/T
40	AC010793	1	90149	F20B17	468443	9738	9740	SNP	1		G/C
40	AC010793	1	90149	F20B17	468614	66111	66113	SNP	1		G/A
40	AC010793	1	90149	F20B17	468615	66328	66330	SNP	1		T/C
40	AC010793	1	90149	F20B17	468616	66363	66365	SNP	1		A/C
40	AC010793	1	90149	F20B17	468617	64989	64991	SNP	1		A/T
40	AC010793	1	90149	F20B17	468618	67511	67513	SNP	1		C/A
40	AC010793	1	90149	F20B17	468619	67619	67621	SNP	1		G/T
40	AC010793	1	90149	F20B17	469288	69928	69930	SNP	1		C/A
40	AC010793	1	90149	F20B17	469862	15301	15312	IND	2	10/-10	
40	AC010793	1	90149	F20B17	469863	47342	47343	IND	2	-3/3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
40	AC010793	1	90149	F20B17	469864	78011	78012	IND	2	-7/7	
40	AC010793	1	90149	F20B17	471206	4771	4772	IND	1	-2/2	
40	AC010793	1	90149	F20B17	471207	57540	57542	IND	1	1/-1	
41	AC006837	2	87584	F23H14	467921	75416	75418	SNP	1		C/A
41	AC006837	2	87584	F23H14	468703	86107	86109	SNP	1		C/A
41	AC006837	2	87584	F23H14	469865	12879	12920	IND	2	40/-40	
41	AC006837	2	87584	F23H14	469866	13133	16333	IND	2	3199/-3199	
41	AC006837	2	87584	F23H14	469867	19400	19401	IND	2	-7/7	
41	AC006837	2	87584	F23H14	469868	22592	22629	IND	2	36/-36	
41	AC006837	2	87584	F23H14	469869	22932	28384	IND	2	5451/-5451	
41	AC006837	2	87584	F23H14	469870	24106	24107	IND	2	-14/14	
41	AC006837	2	87584	F23H14	469871	26527	26528	IND	2	-4/4	
41	AC006837	2	87584	F23H14	469872	28142	42196	IND	2	14053/-14053	
41	AC006837	2	87584	F23H14	469873	47873	47874	IND	2	-4/4	
41	AC006837	2	87584	F23H14	469874	61687	64076	IND	2	2388/-2388	
41	AC006837	2	87584	F23H14	469875	62060	62061	IND	2	-4/4	
41	AC006837	2	87584	F23H14	469876	62720	62751	IND	2	30/-30	
41	AC006837	2	87584	F23H14	469877	82080	82090	IND	2	9/-9	
42	AC007730	2	94503	T5M2	471731	10774	10776	SNP	1		G/A
42	AC007730	2	94503	T5M2	471732	10426	10428	SNP	1		A/C
42	AC007730	2	94503	T5M2	471733	10465	10467	SNP	1		A/C
42	AC007730	2	94503	T5M2	471734	10332	10334	SNP	1		C/G
42	AC007730	2	94503	T5M2	471735	10360	10362	SNP	1		C/T
42	AC007730	2	94503	T5M2	471736	10623	10625	SNP	1		A/T
43	AC007584	2	82189	MJB20	472107	54110	54112	SNP	1		T/A
43	AC007584	2	82189	MJB20	472164	71962	71964	SNP	1		A/C
43	AC007584	2	82189	MJB20	472165	72086	72088	SNP	1		A/C
43	AC007584	2	82189	MJB20	472166	72157	72159	SNP	1		T/C
43	AC007584	2	82189	MJB20	472167	71699	71701	SNP	1		C/T
43	AC007584	2	82189	MJB20	472170	34565	34567	SNP	1		A/T
43	AC007584	2	82189	MJB20	472435	32756	32758	SNP	1		T/A
43	AC007584	2	82189	MJB20	473109	17169	17171	SNP	1		G/A
43	AC007584	2	82189	MJB20	473289	36224	36226	SNP	1		A/T
43	AC007584	2	82189	MJB20	473959	7296	7300	IND	2	3/-3	
43	AC007584	2	82189	MJB20	474351	2074	2075	IND	1	-1/1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
43	AC007584	2	82189	MJB20	474352	53755	53757	IND	1	1/-1	
44	AC007509	2	11178	T19E12	473036	7202	7204	SNP	1		A/C
45	AC018721	2	57991	T7M7	472041	21546	21548	SNP	1		G/C
45	AC018721	2	57991	T7M7	472294	25181	25183	SNP	1		T/C
45	AC018721	2	57991	T7M7	472349	24282	24284	SNP	1		T/G
45	AC018721	2	57991	T7M7	472350	24281	24283	SNP	1		C/T
45	AC018721	2	57991	T7M7	472437	27214	27216	SNP	1		T/C
45	AC018721	2	57991	T7M7	472438	26803	26805	SNP	1		A/G
45	AC018721	2	57991	T7M7	472439	27002	27004	SNP	1		A/T
45	AC018721	2	57991	T7M7	472440	27784	27786	SNP	1		G/T
45	AC018721	2	57991	T7M7	472833	34750	34752	SNP	1		A/G
45	AC018721	2	57991	T7M7	472874	57256	57258	SNP	1		A/G
45	AC018721	2	57991	T7M7	472949	31600	31602	SNP	1		T/A
45	AC018721	2	57991	T7M7	472950	31355	31357	SNP	1		G/C
45	AC018721	2	57991	T7M7	472997	30473	30475	SNP	1		T/G
45	AC018721	2	57991	T7M7	473167	36545	36547	SNP	1		T/G
45	AC018721	2	57991	T7M7	474033	18789	18799	IND	2	9/-9	
45	AC018721	2	57991	T7M7	474034	19795	19796	IND	2	-5/5	
45	AC018721	2	57991	T7M7	474035	2295	2323	IND	2	27/-27	
45	AC018721	2	57991	T7M7	474036	23057	23062	IND	2	4/-4	
45	AC018721	2	57991	T7M7	474037	2640	2641	IND	2	-4/4	
45	AC018721	2	57991	T7M7	474038	2924	2928	IND	2	3/-3	
45	AC018721	2	57991	T7M7	474039	3324	3325	IND	2	-14/14	
45	AC018721	2	57991	T7M7	474040	53773	53779	IND	2	5/-5	
45	AC018721	2	57991	T7M7	474041	53789	53790	IND	2	-4/4	
45	AC018721	2	57991	T7M7	474476	32206	35559	IND	1	-1/1	
46	AC008261	3	93735	T4P13	472295	84815	84817	SNP	1		T/A
46	AC008261	3	93735	T4P13	472296	85689	85691	SNP	1		A/G
46	AC008261	3	93735	T4P13	472297	82280	82282	SNP	1		G/A
46	AC008261	3	93735	T4P13	472298	81447	81449	SNP	1		C/A
46	AC008261	3	93735	T4P13	472299	82925	82927	SNP	1		C/G
46	AC008261	3	93735	T4P13	472300	80654	80656	SNP	1		A/G
46	AC008261	3	93735	T4P13	472301	82826	82828	SNP	1		C/T
46	AC008261	3	93735	T4P13	472302	81407	81409	SNP	1		C/T
46	AC008261	3	93735	T4P13	472332	36816	36818	SNP	1		G/A
46	AC008261	3	93735	T4P13	472333	37002	37004	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
46	AC008261	3	93735	T4P13	472338	56999	57001	SNP	1		T/A
46	AC008261	3	93735	T4P13	472339	57540	57542	SNP	1		T/C
46	AC008261	3	93735	T4P13	472362	77095	77097	SNP	1		C/G
46	AC008261	3	93735	T4P13	472785	42782	42784	SNP	1		T/G
46	AC008261	3	93735	T4P13	472786	42813	42815	SNP	1		A/G
46	AC008261	3	93735	T4P13	472787	42697	42699	SNP	1		C/T
46	AC008261	3	93735	T4P13	472816	78034	78036	SNP	1		C/T
46	AC008261	3	93735	T4P13	472892	27224	27226	SNP	1		G/T
46	AC008261	3	93735	T4P13	472935	30744	30746	SNP	1		A/T
46	AC008261	3	93735	T4P13	473003	16549	16551	SNP	1		T/C
46	AC008261	3	93735	T4P13	473004	16699	16701	SNP	1		C/G
46	AC008261	3	93735	T4P13	473005	16536	16538	SNP	1		C/T
46	AC008261	3	93735	T4P13	473006	16446	16448	SNP	1		A/T
46	AC008261	3	93735	T4P13	473128	89386	89388	SNP	1		A/G
46	AC008261	3	93735	T4P13	473464	69005	69007	SNP	1		G/A
46	AC008261	3	93735	T4P13	473465	71120	71122	SNP	1		C/A
46	AC008261	3	93735	T4P13	473466	68558	68560	SNP	1		T/C
46	AC008261	3	93735	T4P13	473467	69750	69752	SNP	1		G/C
46	AC008261	3	93735	T4P13	473468	71026	71028	SNP	1		T/C
46	AC008261	3	93735	T4P13	473498	28969	28971	SNP	1		G/A
46	AC008261	3	93735	T4P13	473499	28925	28927	SNP	1		A/G
46	AC008261	3	93735	T4P13	473500	28989	28991	SNP	1		C/T
46	AC008261	3	93735	T4P13	473503	66450	66452	SNP	1		G/C
46	AC008261	3	93735	T4P13	473504	66981	66983	SNP	1		A/T
46	AC008261	3	93735	T4P13	473701	35075	35077	SNP	1		G/A
46	AC008261	3	93735	T4P13	474462	30774	30775	IND	1	-4/4	
46	AC008261	3	93735	T4P13	474463	32903	32905	IND	1	1/-1	
46	AC008261	3	93735	T4P13	474464	35558	35559	IND	1	-1/1	
46	AC008261	3	93735	T4P13	474465	42758	42759	IND	1	-1/1	
46	AC008261	3	93735	T4P13	474466	45921	45923	IND	1	1/-1	
46	AC008261	3	93735	T4P13	474467	65784	65786	IND	1	1/-1	
46	AC008261	3	93735	T4P13	474468	66185	66187	IND	1	1/-1	
46	AC008261	3	93735	T4P13	474469	66433	66434	IND	1	-1/1	
46	AC008261	3	93735	T4P13	474470	66561	66562	IND	1	-2/2	
46	AC008261	3	93735	T4P13	474471	70420	70421	IND	1	-1/1	
46	AC008261	3	93735	T4P13	474472	70996	70997	IND	1	-1/1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
46	AC008261	3	93735	T4P13	474473	71084	71087	IND	1	2/-2	
46	AC008261	3	93735	T4P13	474474	82362	82363	IND	1	-1/1	
46	AC008261	3	93735	T4P13	474475	84001	84002	IND	1	-1/1	
47	AC009177	3	140064	T12H1	466885	10794	10796	SNP	1		C/A
47	AC009177	3	140064	T12H1	466963	49030	49032	SNP	1		A/G
47	AC009177	3	140064	T12H1	466998	77467	77469	SNP	1		C/T
47	AC009177	3	140064	T12H1	467131	15173	15175	SNP	1		A/T
47	AC009177	3	140064	T12H1	467132	16021	16023	SNP	1		T/C
47	AC009177	3	140064	T12H1	467133	15318	15320	SNP	1		A/G
47	AC009177	3	140064	T12H1	467134	15132	15134	SNP	1		T/G
47	AC009177	3	140064	T12H1	467135	14555	14557	SNP	1		A/G
47	AC009177	3	140064	T12H1	467136	16018	16020	SNP	1		A/T
47	AC009177	3	140064	T12H1	467181	127043	127045	SNP	1		T/A
47	AC009177	3	140064	T12H1	467182	126524	126526	SNP	1		T/C
47	AC009177	3	140064	T12H1	467183	126532	126534	SNP	1		C/G
47	AC009177	3	140064	T12H1	467184	127465	127467	SNP	1		A/G
47	AC009177	3	140064	T12H1	467185	127065	127067	SNP	1		T/G
47	AC009177	3	140064	T12H1	467367	34114	34116	SNP	1		A/C
47	AC009177	3	140064	T12H1	467368	32828	32830	SNP	1		G/C
47	AC009177	3	140064	T12H1	467442	58167	58169	SNP	1		G/C
47	AC009177	3	140064	T12H1	467493	19930	19932	SNP	1		C/G
47	AC009177	3	140064	T12H1	467512	35723	35725	SNP	1		T/A
47	AC009177	3	140064	T12H1	467513	36156	36158	SNP	1		T/C
47	AC009177	3	140064	T12H1	467514	36308	36310	SNP	1		A/G
47	AC009177	3	140064	T12H1	467579	17857	17859	SNP	1		G/A
47	AC009177	3	140064	T12H1	467580	17257	17259	SNP	1		C/A
47	AC009177	3	140064	T12H1	467581	17211	17213	SNP	1		C/A
47	AC009177	3	140064	T12H1	467582	17403	17405	SNP	1		A/C
47	AC009177	3	140064	T12H1	467583	17525	17527	SNP	1		C/T
47	AC009177	3	140064	T12H1	467584	17399	17401	SNP	1		A/T
47	AC009177	3	140064	T12H1	467631	93276	93278	SNP	1		C/A
47	AC009177	3	140064	T12H1	467632	92941	92943	SNP	1		A/C
47	AC009177	3	140064	T12H1	467633	90685	90687	SNP	1		A/G
47	AC009177	3	140064	T12H1	467634	91582	91584	SNP	1		C/T
47	AC009177	3	140064	T12H1	467682	1005	1007	SNP	1		T/G
47	AC009177	3	140064	T12H1	467683	1734	1736	SNP	1		G/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
47	AC009177	3	140064	T12H1	467684	2975	2977	SNP	1		A/C
47	AC009177	3	140064	T12H1	467685	2535	2537	SNP	1		A/G
47	AC009177	3	140064	T12H1	467837	86013	86015	SNP	1		G/T
47	AC009177	3	140064	T12H1	467838	85650	85652	SNP	1		C/T
47	AC009177	3	140064	T12H1	467976	67616	67618	SNP	1		T/A
47	AC009177	3	140064	T12H1	467977	68901	68903	SNP	1		C/T
47	AC009177	3	140064	T12H1	468311	9780	9782	SNP	1		A/C
47	AC009177	3	140064	T12H1	468312	9781	9783	SNP	1		A/C
47	AC009177	3	140064	T12H1	468324	65178	65180	SNP	1		C/T
47	AC009177	3	140064	T12H1	468485	79431	79433	SNP	1		A/G
47	AC009177	3	140064	T12H1	468641	107256	107258	SNP	1		G/C
47	AC009177	3	140064	T12H1	468668	135451	135453	SNP	1		T/G
47	AC009177	3	140064	T12H1	468934	12027	12029	SNP	1		G/A
47	AC009177	3	140064	T12H1	468935	11409	11411	SNP	1		T/A
47	AC009177	3	140064	T12H1	468936	11408	11410	SNP	1		A/T
47	AC009177	3	140064	T12H1	470578	136121	136122	IND	2	-3/3	
47	AC009177	3	140064	T12H1	470579	136131	136145	IND	2	13/-13	
47	AC009177	3	140064	T12H1	470580	17838	17843	IND	2	4/-4	
47	AC009177	3	140064	T12H1	470581	4191	4434	IND	2	242/-242	
47	AC009177	3	140064	T12H1	470582	52284	52288	IND	2	3/-3	
47	AC009177	3	140064	T12H1	470583	52334	52335	IND	2	-15/15	
47	AC009177	3	140064	T12H1	470584	75253	75259	IND	2	5/-5	
47	AC009177	3	140064	T12H1	470585	77771	77775	IND	2	3/-3	
47	AC009177	3	140064	T12H1	470586	87754	87758	IND	2	3/-3	
47	AC009177	3	140064	T12H1	470587	96207	96208	IND	2	-9/9	
47	AC009177	3	140064	T12H1	470588	96208	96209	IND	2	-9/9	
47	AC009177	3	140064	T12H1	471423	115172	115173	IND	1	-1/1	
47	AC009177	3	140064	T12H1	471424	16515	16516	IND	1	-1/1	
47	AC009177	3	140064	T12H1	471425	17261	17262	IND	1	-2/2	
47	AC009177	3	140064	T12H1	471426	17844	17848	IND	1	3/-3	
47	AC009177	3	140064	T12H1	471427	17851	17853	IND	1	1/-1	
47	AC009177	3	140064	T12H1	471428	91425	91426	IND	1	-2/2	
47	AC009177	3	140064	T12H1	471429	92615	92616	IND	1	-2/2	
47	AC009177	3	140064	T12H1	471430	9773	9777	IND	1	3/-3	
47	AC009177	3	140064	T12H1	471431	9785	9787	IND	1	1/-1	
48	AC009606	3	91924	F22F7	471695	85651	85653	SNP	1		C/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
48	AC009606	3	91924	F22F7	471696	85515	85517	SNP	1		G/A
48	AC009606	3	91924	F22F7	471697	85718	85720	SNP	1		G/C
48	AC009606	3	91924	F22F7	471698	85557	85559	SNP	1		T/C
48	AC009606	3	91924	F22F7	471699	85735	85737	SNP	1		T/G
48	AC009606	3	91924	F22F7	471700	85602	85604	SNP	1		T/G
48	AC009606	3	91924	F22F7	471701	85531	85533	SNP	1		T/G
48	AC009606	3	91924	F22F7	471702	85547	85549	SNP	1		C/T
48	AC009606	3	91924	F22F7	472171	45471	45473	SNP	1		T/A
48	AC009606	3	91924	F22F7	472172	45815	45817	SNP	1		A/T
48	AC009606	3	91924	F22F7	472323	90310	90312	SNP	1		G/C
48	AC009606	3	91924	F22F7	472324	89377	89379	SNP	1		T/C
48	AC009606	3	91924	F22F7	472325	89777	89779	SNP	1		A/C
48	AC009606	3	91924	F22F7	472326	90318	90320	SNP	1		A/G
48	AC009606	3	91924	F22F7	472327	89799	89801	SNP	1		A/T
48	AC009606	3	91924	F22F7	472466	52893	52895	SNP	1		G/A
48	AC009606	3	91924	F22F7	472467	52824	52826	SNP	1		A/C
48	AC009606	3	91924	F22F7	472482	31400	31402	SNP	1		A/C
48	AC009606	3	91924	F22F7	472636	72854	72856	SNP	1		C/A
48	AC009606	3	91924	F22F7	472637	72793	72795	SNP	1		G/C
48	AC009606	3	91924	F22F7	472638	72748	72750	SNP	1		T/C
48	AC009606	3	91924	F22F7	472639	72689	72691	SNP	1		A/C
48	AC009606	3	91924	F22F7	472640	72875	72877	SNP	1		A/G
48	AC009606	3	91924	F22F7	472641	72270	72272	SNP	1		A/T
48	AC009606	3	91924	F22F7	472642	72864	72866	SNP	1		A/T
48	AC009606	3	91924	F22F7	472733	54586	54588	SNP	1		C/T
48	AC009606	3	91924	F22F7	472734	56723	56725	SNP	1		G/A
48	AC009606	3	91924	F22F7	472735	56728	56730	SNP	1		T/A
48	AC009606	3	91924	F22F7	472736	55491	55493	SNP	1		G/A
48	AC009606	3	91924	F22F7	472737	56722	56724	SNP	1		A/G
48	AC009606	3	91924	F22F7	472738	55899	55901	SNP	1		A/G
48	AC009606	3	91924	F22F7	473152	39785	39787	SNP	1		T/C
48	AC009606	3	91924	F22F7	473360	81391	81393	SNP	1		A/C
48	AC009606	3	91924	F22F7	473368	5548	5550	SNP	1		A/C
48	AC009606	3	91924	F22F7	473369	5034	5036	SNP	1		T/C
48	AC009606	3	91924	F22F7	473370	5507	5509	SNP	1		G/T
48	AC009606	3	91924	F22F7	473371	5446	5448	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
48	AC009606	3	91924	F22F7	473372	5298	5300	SNP	1		A/T
48	AC009606	3	91924	F22F7	473515	74551	74553	SNP	1		C/A
48	AC009606	3	91924	F22F7	473534	11152	11154	SNP	1		T/G
48	AC009606	3	91924	F22F7	473657	53947	53949	SNP	1		T/C
48	AC009606	3	91924	F22F7	473795	38189	38191	SNP	1		A/T
48	AC009606	3	91924	F22F7	473856	17377	17389	IND	2	11/-11	
48	AC009606	3	91924	F22F7	473857	27894	27901	IND	2	6/-6	
48	AC009606	3	91924	F22F7	473858	28944	28945	IND	2	-3/3	
48	AC009606	3	91924	F22F7	473859	32049	32050	IND	2	-4/4	
48	AC009606	3	91924	F22F7	473860	35041	35059	IND	2	17/-17	
48	AC009606	3	91924	F22F7	473861	3531	3532	IND	2	-6/6	
48	AC009606	3	91924	F22F7	473862	36309	36310	IND	2	-4/4	
48	AC009606	3	91924	F22F7	473863	37931	37997	IND	2	65/-65	
48	AC009606	3	91924	F22F7	473864	43375	43376	IND	2	-4/4	
48	AC009606	3	91924	F22F7	473865	46575	46576	IND	2	-3/3	
48	AC009606	3	91924	F22F7	474110	32051	32052	IND	1	-1/1	
48	AC009606	3	91924	F22F7	474111	32052	32053	IND	1	-1/1	
48	AC009606	3	91924	F22F7	474112	32053	32054	IND	1	-2/2	
48	AC009606	3	91924	F22F7	474113	5262	5265	IND	1	2/-2	
48	AC009606	3	91924	F22F7	474114	56281	56283	IND	1	1/-1	
48	AC009606	3	91924	F22F7	474115	70536	70538	IND	1	1/-1	
48	AC009606	3	91924	F22F7	474116	72672	72674	IND	1	1/-1	
48	AC009606	3	91924	F22F7	474117	72767	72770	IND	1	2/-2	
49	AC009176	3	79296	MLP3	470452	10508	10512	IND	2	3/-3	
49	AC009176	3	79296	MLP3	470453	11763	11767	IND	2	3/-3	
49	AC009176	3	79296	MLP3	470454	13024	13025	IND	2	-3/3	
49	AC009176	3	79296	MLP3	470455	13235	13236	IND	2	-13/13	
49	AC009176	3	79296	MLP3	470456	37818	37819	IND	2	-88/88	
49	AC009176	3	79296	MLP3	470457	42038	42042	IND	2	3/-3	
49	AC009176	3	79296	MLP3	470458	58930	58935	IND	2	4/-4	
49	AC009176	3	79296	MLP3	470459	58936	58941	IND	2	4/-4	
49	AC009176	3	79296	MLP3	470460	62240	62245	IND	2	4/-4	
49	AC009176	3	79296	MLP3	470461	78114	78137	IND	2	22/-22	
49	AC009176	3	79296	MLP3	470462	78492	78493	IND	2	-3/3	
49	AC009176	3	79296	MLP3	470463	8447	8448	IND	2	-8/8	
49	AC009176	3	79296	MLP3	470464	8718	8719	IND	2	-12/12	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
50	AB028610	3	38810	MCP4	466918	22733	22735	SNP	1		T/C
50	AB028610	3	38810	MCP4	466919	23110	23112	SNP	1		A/C
50	AB028610	3	38810	MCP4	466920	23480	23482	SNP	1		A/G
50	AB028610	3	38810	MCP4	466921	23079	23081	SNP	1		A/G
50	AB028610	3	38810	MCP4	468147	5441	5443	SNP	1		G/A
50	AB028610	3	38810	MCP4	468148	5730	5732	SNP	1		C/A
50	AB028610	3	38810	MCP4	468149	5731	5733	SNP	1		A/C
50	AB028610	3	38810	MCP4	468150	5739	5741	SNP	1		A/G
50	AB028610	3	38810	MCP4	468151	5735	5737	SNP	1		A/G
50	AB028610	3	38810	MCP4	468308	34494	34496	SNP	1		C/A
50	AB028610	3	38810	MCP4	468613	4700	4702	SNP	1		A/G
50	AB028610	3	38810	MCP4	469138	28894	28896	SNP	1		T/C
50	AB028610	3	38810	MCP4	469139	28298	28300	SNP	1		T/G
50	AB028610	3	38810	MCP4	469140	26805	26807	SNP	1		G/T
50	AB028610	3	38810	MCP4	470401	12201	12202	IND	2	-4/4	
50	AB028610	3	38810	MCP4	470402	14410	14411	IND	2	-9/9	
50	AB028610	3	38810	MCP4	470403	1480	1488	IND	2	7/-7	
50	AB028610	3	38810	MCP4	470404	16789	16790	IND	2	-4/4	
50	AB028610	3	38810	MCP4	470405	17079	17080	IND	2	-3/3	
50	AB028610	3	38810	MCP4	470406	7504	7523	IND	2	18/-18	
50	AB028610	3	38810	MCP4	471381	12203	12204	IND	1	-2/2	
51	AB028617	3	52232	MOA2	468109	38039	38041	SNP	1		G/A
51	AB028617	3	52232	MOA2	468110	37929	37931	SNP	1		T/C
51	AB028617	3	52232	MOA2	468111	38244	38246	SNP	1		A/C
51	AB028617	3	52232	MOA2	468267	30182	30184	SNP	1		C/T
51	AB028617	3	52232	MOA2	469006	42048	42050	SNP	1		T/C
51	AB028617	3	52232	MOA2	469007	42095	42097	SNP	1		C/T
51	AB028617	3	52232	MOA2	470473	42556	42569	IND	2	12/-12	
51	AB028617	3	52232	MOA2	470474	42981	42982	IND	2	-9/9	
51	AB028617	3	52232	MOA2	470475	43006	43011	IND	2	4/-4	
51	AB028617	3	52232	MOA2	470476	43046	43047	IND	2	-10/10	
51	AB028617	3	52232	MOA2	470477	43137	43141	IND	2	3/-3	
51	AB028617	3	52232	MOA2	470478	43432	49707	IND	2	6274/-6274	
51	AB028617	3	52232	MOA2	470479	47092	47093	IND	2	-4/4	
51	AB028617	3	52232	MOA2	470480	47093	47094	IND	2	-4/4	
51	AB028617	3	52232	MOA2	470481	47480	47489	IND	2	8/-8	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
51	AB028617	3	52232	MOA2	470482	48877	48886	IND	2	8/-8	
51	AB028617	3	52232	MOA2	470483	48981	48989	IND	2	7/-7	
51	AB028617	3	52232	MOA2	470484	49112	49119	IND	2	6/-6	
51	AB028617	3	52232	MOA2	470485	51109	51110	IND	2	-3/3	
51	AB028617	3	52232	MOA2	470486	51112	51113	IND	2	-3/3	
51	AB028617	3	52232	MOA2	470487	5722	5732	IND	2	9/-9	
51	AB028617	3	52232	MOA2	471384	26250	26252	IND	1	1/-1	
51	AB028617	3	52232	MOA2	471385	41899	41900	IND	1	-1/1	
51	AB028617	3	52232	MOA2	471386	42190	42192	IND	1	1/-1	
52	AB028619	3	22199	MQD17	466800	3176	3178	SNP	1		C/T
52	AB028619	3	22199	MQD17	467198	1926	1928	SNP	1		T/C
52	AB028619	3	22199	MQD17	468112	4379	4381	SNP	1		A/C
52	AB028619	3	22199	MQD17	468676	7894	7896	SNP	1		C/A
52	AB028619	3	22199	MQD17	468677	8665	8667	SNP	1		T/A
52	AB028619	3	22199	MQD17	470501	10743	10744	IND	2	-44/44	
52	AB028619	3	22199	MQD17	470502	10752	10753	IND	2	-44/44	
52	AB028619	3	22199	MQD17	470503	10797	12019	IND	2	1221/-1221	
52	AB028619	3	22199	MQD17	470504	13068	13077	IND	2	8/-8	
52	AB028619	3	22199	MQD17	470505	13635	13636	IND	2	-13/13	
52	AB028619	3	22199	MQD17	470506	13636	13637	IND	2	-13/13	
52	AB028619	3	22199	MQD17	470507	14905	14988	IND	2	82/-82	
52	AB028619	3	22199	MQD17	470508	9576	9577	IND	2	-4/4	
52	AB028619	3	22199	MQD17	471387	4282	4283	IND	1	-1/1	
53	AB028608	3	43500	K20I9	471679	14924	14926	SNP	1		G/C
53	AB028608	3	43500	K20I9	471680	14907	14909	SNP	1		A/C
53	AB028608	3	43500	K20I9	471681	14961	14963	SNP	1		A/G
53	AB028608	3	43500	K20I9	471819	1303	1305	SNP	1		T/G
53	AB028608	3	43500	K20I9	471945	15840	15842	SNP	1		T/C
53	AB028608	3	43500	K20I9	471946	15807	15809	SNP	1		T/G
53	AB028608	3	43500	K20I9	472090	20140	20142	SNP	1		T/C
53	AB028608	3	43500	K20I9	472091	18231	18233	SNP	1		C/T
53	AB028608	3	43500	K20I9	472424	9246	9248	SNP	1		G/A
53	AB028608	3	43500	K20I9	472834	21186	21188	SNP	1		T/A
53	AB028608	3	43500	K20I9	472835	21123	21125	SNP	1		A/T
53	AB028608	3	43500	K20I9	473130	42933	42935	SNP	1		T/A
53	AB028608	3	43500	K20I9	473259	7331	7333	SNP	1		A/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
53	AB028608	3	43500	K20I9	473734	29422	29424	SNP	1		A/C
53	AB028608	3	43500	K20I9	474314	12416	12418	IND	1	1/-1	
53	AB028608	3	43500	K20I9	474315	42983	42984	IND	1	-1/1	
53	AB028608	3	43500	K20I9	474316	42984	42985	IND	1	-1/1	
53	AB028608	3	43500	K20I9	474317	42987	42988	IND	1	-4/4	
54	AB028620	3	19801	MTO12	467314	4661	4663	SNP	1		G/C
54	AB028620	3	19801	MTO12	470510	12278	12287	IND	2	8/-8	
54	AB028620	3	19801	MTO12	470511	12346	12347	IND	2	-5/5	
54	AB028620	3	19801	MTO12	470512	7764	7765	IND	2	-46/46	
55	AP001303	3	45292	K24M9	471704	42031	42033	SNP	1		C/G
55	AP001303	3	45292	K24M9	472116	30926	30928	SNP	1		T/C
55	AP001303	3	45292	K24M9	472587	23049	23051	SNP	1		C/A
55	AP001303	3	45292	K24M9	472705	25994	25996	SNP	1		G/A
55	AP001303	3	45292	K24M9	472706	24989	24991	SNP	1		T/C
55	AP001303	3	45292	K24M9	472707	25837	25839	SNP	1		C/T
55	AP001303	3	45292	K24M9	473538	24316	24318	SNP	1		T/A
55	AP001303	3	45292	K24M9	473539	24347	24349	SNP	1		A/G
55	AP001303	3	45292	K24M9	473640	195	197	SNP	1		A/C
55	AP001303	3	45292	K24M9	473641	780	782	SNP	1		C/T
55	AP001303	3	45292	K24M9	473941	502	503	IND	2	-78/78	
55	AP001303	3	45292	K24M9	474319	1010	1011	IND	1	-2/2	
55	AP001303	3	45292	K24M9	474320	17503	17504	IND	1	-1/1	
55	AP001303	3	45292	K24M9	474321	24169	24170	IND	1	-1/1	
55	AP001303	3	45292	K24M9	474322	24176	24177	IND	1	-2/2	
55	AP001303	3	45292	K24M9	474323	24225	24226	IND	1	-1/1	
55	AP001303	3	45292	K24M9	474324	24233	24236	IND	1	2/-2	
55	AP001303	3	45292	K24M9	474325	38229	38230	IND	1	-2/2	
56	AP000417	3	73977	MMB12	471928	30682	30684	SNP	1		T/C
56	AP000417	3	73977	MMB12	472065	66244	66246	SNP	1		T/A
56	AP000417	3	73977	MMB12	472066	66080	66082	SNP	1		G/C
56	AP000417	3	73977	MMB12	472108	47887	47889	SNP	1		A/G
56	AP000417	3	73977	MMB12	472124	21842	21844	SNP	1		T/A
56	AP000417	3	73977	MMB12	472125	21815	21817	SNP	1		T/A
56	AP000417	3	73977	MMB12	472126	21768	21770	SNP	1		G/A
56	AP000417	3	73977	MMB12	472127	21723	21725	SNP	1		T/A
56	AP000417	3	73977	MMB12	472128	20915	20917	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
56	AP000417	3	73977	MMB12	472129	25386	25388	SNP	1		C/A
56	AP000417	3	73977	MMB12	472130	23432	23434	SNP	1		T/C
56	AP000417	3	73977	MMB12	472131	23431	23433	SNP	1		T/C
56	AP000417	3	73977	MMB12	472132	22953	22955	SNP	1		T/C
56	AP000417	3	73977	MMB12	472133	22028	22030	SNP	1		T/C
56	AP000417	3	73977	MMB12	472134	21998	22000	SNP	1		A/C
56	AP000417	3	73977	MMB12	472135	21995	21997	SNP	1		T/C
56	AP000417	3	73977	MMB12	472136	21863	21865	SNP	1		A/C
56	AP000417	3	73977	MMB12	472137	21670	21672	SNP	1		T/C
56	AP000417	3	73977	MMB12	472138	25894	25896	SNP	1		A/G
56	AP000417	3	73977	MMB12	472139	22439	22441	SNP	1		A/G
56	AP000417	3	73977	MMB12	472140	22030	22032	SNP	1		T/G
56	AP000417	3	73977	MMB12	472141	21929	21931	SNP	1		A/G
56	AP000417	3	73977	MMB12	472142	21921	21923	SNP	1		T/G
56	AP000417	3	73977	MMB12	472143	21705	21707	SNP	1		A/G
56	AP000417	3	73977	MMB12	472144	21686	21688	SNP	1		T/G
56	AP000417	3	73977	MMB12	472145	25190	25192	SNP	1		C/T
56	AP000417	3	73977	MMB12	472146	25075	25077	SNP	1		A/T
56	AP000417	3	73977	MMB12	472147	22108	22110	SNP	1		A/T
56	AP000417	3	73977	MMB12	472148	21881	21883	SNP	1		A/T
56	AP000417	3	73977	MMB12	472149	21720	21722	SNP	1		A/T
56	AP000417	3	73977	MMB12	472150	21712	21714	SNP	1		A/T
56	AP000417	3	73977	MMB12	472151	25363	25365	SNP	1		A/T
56	AP000417	3	73977	MMB12	472168	69097	69099	SNP	1		C/A
56	AP000417	3	73977	MMB12	472169	68254	68256	SNP	1		T/C
56	AP000417	3	73977	MMB12	472181	28854	28856	SNP	1		G/A
56	AP000417	3	73977	MMB12	472182	28870	28872	SNP	1		G/A
56	AP000417	3	73977	MMB12	472391	48273	48275	SNP	1		G/A
56	AP000417	3	73977	MMB12	472425	14379	14381	SNP	1		T/A
56	AP000417	3	73977	MMB12	472469	32811	32813	SNP	1		A/T
56	AP000417	3	73977	MMB12	472477	6783	6785	SNP	1		A/G
56	AP000417	3	73977	MMB12	472493	59990	59992	SNP	1		T/C
56	AP000417	3	73977	MMB12	472507	62562	62564	SNP	1		T/C
56	AP000417	3	73977	MMB12	472508	62198	62200	SNP	1		C/T
56	AP000417	3	73977	MMB12	472564	40402	40404	SNP	1		C/T
56	AP000417	3	73977	MMB12	472585	69560	69562	SNP	1		T/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
56	AP000417	3	73977	MMB12	472586	70623	70625	SNP	1		C/G
56	AP000417	3	73977	MMB12	473033	27616	27618	SNP	1		T/G
56	AP000417	3	73977	MMB12	473034	27606	27608	SNP	1		G/T
56	AP000417	3	73977	MMB12	473035	27630	27632	SNP	1		G/T
56	AP000417	3	73977	MMB12	473304	50622	50624	SNP	1		C/A
56	AP000417	3	73977	MMB12	473651	38998	39000	SNP	1		G/A
56	AP000417	3	73977	MMB12	473652	39632	39634	SNP	1		T/G
56	AP000417	3	73977	MMB12	473793	41058	41060	SNP	1		G/A
56	AP000417	3	73977	MMB12	473804	13444	13446	SNP	1		G/C
56	AP000417	3	73977	MMB12	473805	12410	12412	SNP	1		G/T
56	AP000417	3	73977	MMB12	473806	12753	12755	SNP	1		C/T
56	AP000417	3	73977	MMB12	473962	11075	11079	IND	2	3/-3	
56	AP000417	3	73977	MMB12	473963	16754	16758	IND	2	3/-3	
56	AP000417	3	73977	MMB12	473964	4723	4724	IND	2	-3/3	
56	AP000417	3	73977	MMB12	474359	22353	22354	IND	1	-1/1	
56	AP000417	3	73977	MMB12	474360	33541	33542	IND	1	-4/4	
56	AP000417	3	73977	MMB12	474361	7061	7062	IND	1	-1/1	
56	AP000417	3	73977	MMB12	474362	7062	7063	IND	1	-1/1	
56	AP000417	3	73977	MMB12	474363	71583	71584	IND	1	-1/1	
57	AP000410	3	55161	K10D20	472061	4316	4318	SNP	1		A/C
57	AP000410	3	55161	K10D20	472062	5082	5084	SNP	1		C/G
57	AP000410	3	55161	K10D20	472063	4250	4252	SNP	1		C/T
57	AP000410	3	55161	K10D20	472064	5080	5082	SNP	1		C/T
57	AP000410	3	55161	K10D20	472290	14932	14934	SNP	1		G/A
57	AP000410	3	55161	K10D20	472291	14895	14897	SNP	1		C/T
57	AP000410	3	55161	K10D20	472292	14910	14912	SNP	1		A/T
57	AP000410	3	55161	K10D20	472664	35285	35287	SNP	1		T/A
57	AP000410	3	55161	K10D20	472665	35257	35259	SNP	1		T/A
57	AP000410	3	55161	K10D20	472666	34975	34977	SNP	1		G/A
57	AP000410	3	55161	K10D20	472667	35253	35255	SNP	1		A/C
57	AP000410	3	55161	K10D20	472668	34993	34995	SNP	1		A/C
57	AP000410	3	55161	K10D20	472669	35284	35286	SNP	1		A/T
57	AP000410	3	55161	K10D20	472670	35036	35038	SNP	1		A/T
57	AP000410	3	55161	K10D20	472671	33872	33874	SNP	1		G/A
57	AP000410	3	55161	K10D20	472672	34175	34177	SNP	1		G/C
57	AP000410	3	55161	K10D20	472673	34342	34344	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
57	AP000410	3	55161	K10D20	472674	34362	34364	SNP	1		A/G
57	AP000410	3	55161	K10D20	472675	34517	34519	SNP	1		A/G
57	AP000410	3	55161	K10D20	473208	11332	11334	SNP	1		T/A
57	AP000410	3	55161	K10D20	473209	11138	11140	SNP	1		T/C
57	AP000410	3	55161	K10D20	473210	11526	11528	SNP	1		A/G
57	AP000410	3	55161	K10D20	473397	53956	53958	SNP	1		T/C
57	AP000410	3	55161	K10D20	473398	54392	54394	SNP	1		C/T
57	AP000410	3	55161	K10D20	473399	53901	53903	SNP	1		C/T
57	AP000410	3	55161	K10D20	473510	40926	40928	SNP	1		C/G
57	AP000410	3	55161	K10D20	473511	40681	40683	SNP	1		C/T
57	AP000410	3	55161	K10D20	473529	16206	16208	SNP	1		T/A
57	AP000410	3	55161	K10D20	473530	16589	16591	SNP	1		C/A
57	AP000410	3	55161	K10D20	473531	16894	16896	SNP	1		G/A
57	AP000410	3	55161	K10D20	473532	15352	15354	SNP	1		T/C
57	AP000410	3	55161	K10D20	473533	15354	15356	SNP	1		A/G
57	AP000410	3	55161	K10D20	473540	39494	39496	SNP	1		G/T
57	AP000410	3	55161	K10D20	473541	39411	39413	SNP	1		A/T
57	AP000410	3	55161	K10D20	473732	18593	18595	SNP	1		C/T
57	AP000410	3	55161	K10D20	473745	37779	37781	SNP	1		C/A
57	AP000410	3	55161	K10D20	473774	13823	13825	SNP	1		G/A
57	AP000410	3	55161	K10D20	473775	13469	13471	SNP	1		C/A
57	AP000410	3	55161	K10D20	473776	13799	13801	SNP	1		A/T
57	AP000410	3	55161	K10D20	473792	27257	27259	SNP	1		G/T
57	AP000410	3	55161	K10D20	473931	15309	15318	IND	2	8/-8	
57	AP000410	3	55161	K10D20	474304	10596	10598	IND	1	1/-1	
57	AP000410	3	55161	K10D20	474305	10878	10879	IND	1	-1/1	
57	AP000410	3	55161	K10D20	474306	14917	14918	IND	1	-2/2	
57	AP000410	3	55161	K10D20	474307	14957	14959	IND	1	1/-1	
57	AP000410	3	55161	K10D20	474308	15327	15329	IND	1	1/-1	
57	AP000410	3	55161	K10D20	474309	16675	16677	IND	1	1/-1	
57	AP000410	3	55161	K10D20	474310	5068	5069	IND	1	-2/2	
58	AP001305	3	58510	MHC9	472039	16830	16832	SNP	1		T/A
58	AP001305	3	58510	MHC9	472040	16706	16708	SNP	1		G/A
58	AP001305	3	58510	MHC9	472072	5656	5658	SNP	1		A/C
58	AP001305	3	58510	MHC9	472073	6229	6231	SNP	1		A/C
58	AP001305	3	58510	MHC9	472074	6010	6012	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
58	AP001305	3	58510	MHC9	472075	5887	5889	SNP	1		T/G
58	AP001305	3	58510	MHC9	472184	37439	37441	SNP	1		T/G
58	AP001305	3	58510	MHC9	472235	36723	36725	SNP	1		C/A
58	AP001305	3	58510	MHC9	472236	36690	36692	SNP	1		T/C
58	AP001305	3	58510	MHC9	472868	41449	41451	SNP	1		A/T
58	AP001305	3	58510	MHC9	472923	31981	31983	SNP	1		C/A
58	AP001305	3	58510	MHC9	472972	25640	25642	SNP	1		A/G
58	AP001305	3	58510	MHC9	472973	25768	25770	SNP	1		G/T
58	AP001305	3	58510	MHC9	473346	19101	19103	SNP	1		C/G
58	AP001305	3	58510	MHC9	473362	51497	51499	SNP	1		C/A
58	AP001305	3	58510	MHC9	473363	51461	51463	SNP	1		C/G
58	AP001305	3	58510	MHC9	473364	50429	50431	SNP	1		A/C
58	AP001305	3	58510	MHC9	473365	50302	50304	SNP	1		T/C
58	AP001305	3	58510	MHC9	473366	50502	50504	SNP	1		G/T
58	AP001305	3	58510	MHC9	473585	23039	23041	SNP	1		G/A
58	AP001305	3	58510	MHC9	473586	23592	23594	SNP	1		C/A
58	AP001305	3	58510	MHC9	473587	23084	23086	SNP	1		A/C
58	AP001305	3	58510	MHC9	473955	21617	21622	IND	2	4/-4	
58	AP001305	3	58510	MHC9	473956	23364	23365	IND	2	-4/4	
58	AP001305	3	58510	MHC9	473957	4415	4416	IND	2	-6/6	
58	AP001305	3	58510	MHC9	473958	529	542	IND	2	12/-12	
58	AP001305	3	58510	MHC9	474343	17569	17570	IND	1	-1/1	
58	AP001305	3	58510	MHC9	474344	21623	21625	IND	1	1/-1	
58	AP001305	3	58510	MHC9	474345	21628	21632	IND	1	3/-3	
58	AP001305	3	58510	MHC9	474346	23363	23364	IND	1	-4/4	
58	AP001305	3	58510	MHC9	474347	23802	23804	IND	1	1/-1	
58	AP001305	3	58510	MHC9	474348	36868	36869	IND	1	-1/1	
58	AP001305	3	58510	MHC9	474349	4427	4428	IND	1	-6/6	
58	AP001305	3	58510	MHC9	474350	48204	48205	IND	1	-4/4	
59	AP000739	3	6184	MEK6	468113	1979	1981	SNP	1		T/G
60	AB028622	3	82348	MZN24	466874	22030	22032	SNP	1		G/A
60	AB028622	3	82348	MZN24	466875	22031	22033	SNP	1		A/T
60	AB028622	3	82348	MZN24	466934	12401	12403	SNP	1		A/G
60	AB028622	3	82348	MZN24	466935	12666	12668	SNP	1		C/T
60	AB028622	3	82348	MZN24	466936	15401	15403	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
60	AB028622	3	82348	MZN24	466937	14339	14341	SNP	1		G/A
60	AB028622	3	82348	MZN24	466938	15222	15224	SNP	1		T/C
60	AB028622	3	82348	MZN24	466939	15723	15725	SNP	1		A/C
60	AB028622	3	82348	MZN24	466940	16084	16086	SNP	1		G/C
60	AB028622	3	82348	MZN24	466941	14998	15000	SNP	1		A/G
60	AB028622	3	82348	MZN24	466942	15400	15402	SNP	1		T/G
60	AB028622	3	82348	MZN24	466943	14713	14715	SNP	1		A/G
60	AB028622	3	82348	MZN24	466944	14958	14960	SNP	1		A/T
60	AB028622	3	82348	MZN24	466945	13979	13981	SNP	1		C/T
60	AB028622	3	82348	MZN24	467657	75590	75592	SNP	1		G/A
60	AB028622	3	82348	MZN24	467658	75533	75535	SNP	1		A/G
60	AB028622	3	82348	MZN24	467659	75464	75466	SNP	1		A/T
60	AB028622	3	82348	MZN24	467706	21020	21022	SNP	1		T/C
60	AB028622	3	82348	MZN24	467707	20837	20839	SNP	1		T/C
60	AB028622	3	82348	MZN24	467812	62314	62316	SNP	1		C/T
60	AB028622	3	82348	MZN24	468400	871	873	SNP	1		G/T
60	AB028622	3	82348	MZN24	468415	19461	19463	SNP	1		T/G
60	AB028622	3	82348	MZN24	468416	19556	19558	SNP	1		A/T
60	AB028622	3	82348	MZN24	468417	19528	19530	SNP	1		C/T
60	AB028622	3	82348	MZN24	468418	33022	33024	SNP	1		T/G
60	AB028622	3	82348	MZN24	468419	23242	23244	SNP	1		G/A
60	AB028622	3	82348	MZN24	468420	23191	23193	SNP	1		A/C
60	AB028622	3	82348	MZN24	468421	23076	23078	SNP	1		A/T
60	AB028622	3	82348	MZN24	468422	23706	23708	SNP	1		C/T
60	AB028622	3	82348	MZN24	468423	23851	23853	SNP	1		C/T
60	AB028622	3	82348	MZN24	468964	46483	46485	SNP	1		G/A
60	AB028622	3	82348	MZN24	468965	46599	46601	SNP	1		A/C
60	AB028622	3	82348	MZN24	468966	46829	46831	SNP	1		A/G
60	AB028622	3	82348	MZN24	468967	45795	45797	SNP	1		C/T
60	AB028622	3	82348	MZN24	469131	55416	55418	SNP	1		G/A
60	AB028622	3	82348	MZN24	470521	18075	18076	IND	2	-4/4	
60	AB028622	3	82348	MZN24	470522	25063	25078	IND	2	14/-14	
60	AB028622	3	82348	MZN24	470523	25582	25583	IND	2	-14/14	
60	AB028622	3	82348	MZN24	470524	41421	41426	IND	2	4/-4	
60	AB028622	3	82348	MZN24	470525	41452	41465	IND	2	12/-12	
60	AB028622	3	82348	MZN24	470526	41503	41504	IND	2	-9/9	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
60	AB028622	3	82348	MZN24	470527	41505	41506	IND	2	-9/9	
60	AB028622	3	82348	MZN24	470528	4194	4908	IND	2	713/-713	
60	AB028622	3	82348	MZN24	470529	42367	57977	IND	2	15609/-15609	
60	AB028622	3	82348	MZN24	470530	49982	49983	IND	2	-9/9	
60	AB028622	3	82348	MZN24	470531	5167	5168	IND	2	-4/4	
60	AB028622	3	82348	MZN24	470532	73430	73431	IND	2	-7/7	
60	AB028622	3	82348	MZN24	471398	15964	15967	IND	1	2/-2	
60	AB028622	3	82348	MZN24	471399	23849	23850	IND	1	-1/1	
60	AB028622	3	82348	MZN24	471400	28446	28447	IND	1	-2/2	
60	AB028622	3	82348	MZN24	471401	33229	33232	IND	1	2/-2	
60	AB028622	3	82348	MZN24	471402	46881	46882	IND	1	-1/1	
60	AB028622	3	82348	MZN24	471403	75603	75605	IND	1	1/-1	
60	AB028622	3	82348	MZN24	471404	886	887	IND	1	-1/1	
61	AP001306	3	70100	MKA23	471727	40287	40289	SNP	1		A/G
61	AP001306	3	70100	MKA23	471864	39454	39456	SNP	1		A/T
61	AP001306	3	70100	MKA23	471869	8811	8813	SNP	1		A/G
61	AP001306	3	70100	MKA23	471870	8922	8924	SNP	1		C/G
61	AP001306	3	70100	MKA23	471871	8735	8737	SNP	1		A/G
61	AP001306	3	70100	MKA23	472191	19148	19150	SNP	1		T/A
61	AP001306	3	70100	MKA23	472192	19430	19432	SNP	1		C/T
61	AP001306	3	70100	MKA23	472207	5291	5293	SNP	1		T/A
61	AP001306	3	70100	MKA23	472208	5355	5357	SNP	1		T/A
61	AP001306	3	70100	MKA23	472209	5279	5281	SNP	1		T/G
61	AP001306	3	70100	MKA23	472210	4940	4942	SNP	1		A/T
61	AP001306	3	70100	MKA23	472591	29527	29529	SNP	1		G/A
61	AP001306	3	70100	MKA23	472592	29488	29490	SNP	1		T/A
61	AP001306	3	70100	MKA23	472593	29478	29480	SNP	1		T/A
61	AP001306	3	70100	MKA23	472594	29603	29605	SNP	1		C/T
61	AP001306	3	70100	MKA23	472595	29529	29531	SNP	1		A/T
61	AP001306	3	70100	MKA23	472596	29513	29515	SNP	1		C/T
61	AP001306	3	70100	MKA23	472951	24555	24557	SNP	1		T/A
61	AP001306	3	70100	MKA23	473357	16441	16443	SNP	1		T/A
61	AP001306	3	70100	MKA23	473358	17080	17082	SNP	1		G/T
61	AP001306	3	70100	MKA23	473441	6169	6171	SNP	1		G/A
61	AP001306	3	70100	MKA23	473442	6291	6293	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
61	AP001306	3	70100	MKA23	473443	6270	6272	SNP	1		A/T
61	AP001306	3	70100	MKA23	473642	33095	33097	SNP	1		T/C
61	AP001306	3	70100	MKA23	473643	33305	33307	SNP	1		A/G
61	AP001306	3	70100	MKA23	473644	33605	33607	SNP	1		A/G
61	AP001306	3	70100	MKA23	473673	60781	60783	SNP	1		C/G
61	AP001306	3	70100	MKA23	473960	14028	14779	IND	2	750/-750	
61	AP001306	3	70100	MKA23	473961	528	529	IND	2	-6/6	
61	AP001306	3	70100	MKA23	474353	1078	1080	IND	1	1/-1	
61	AP001306	3	70100	MKA23	474354	2698	2700	IND	1	1/-1	
61	AP001306	3	70100	MKA23	474355	39465	39466	IND	1	-1/1	
61	AP001306	3	70100	MKA23	474356	5298	5300	IND	1	1/-1	
61	AP001306	3	70100	MKA23	474357	5301	5302	IND	1	-1/1	
61	AP001306	3	70100	MKA23	474358	5312	5314	IND	1	1/-1	
62	AP000731	3	47827	F16J14	471654	9685	9687	SNP	1		T/C
62	AP000731	3	47827	F16J14	471852	7043	7045	SNP	1		A/G
62	AP000731	3	47827	F16J14	472036	38288	38290	SNP	1		G/A
62	AP000731	3	47827	F16J14	472037	38724	38726	SNP	1		T/G
62	AP000731	3	47827	F16J14	472038	38919	38921	SNP	1		A/T
62	AP000731	3	47827	F16J14	472102	2701	2703	SNP	1		G/A
62	AP000731	3	47827	F16J14	472561	43629	43631	SNP	1		C/T
62	AP000731	3	47827	F16J14	472776	46626	46628	SNP	1		T/A
62	AP000731	3	47827	F16J14	472777	46490	46492	SNP	1		T/G
62	AP000731	3	47827	F16J14	473115	11635	11637	SNP	1		T/C
62	AP000731	3	47827	F16J14	473367	45139	45141	SNP	1		T/A
62	AP000731	3	47827	F16J14	473677	6042	6044	SNP	1		T/A
62	AP000731	3	47827	F16J14	473678	6359	6361	SNP	1		A/C
62	AP000731	3	47827	F16J14	473838	16168	16172	IND	2	3/-3	
62	AP000731	3	47827	F16J14	473839	440	463	IND	2	22/-22	
62	AP000731	3	47827	F16J14	473840	8898	8903	IND	2	4/-4	
62	AP000731	3	47827	F16J14	473841	9449	9450	IND	2	-6/6	
62	AP000731	3	47827	F16J14	474072	26474	26475	IND	1	-1/1	
62	AP000731	3	47827	F16J14	474073	27909	27910	IND	1	-1/1	
62	AP000731	3	47827	F16J14	474074	30219	30220	IND	1	-5/5	
63	AP001300	3	71327	F5N5	471728	49537	49539	SNP	1		G/A
63	AP001300	3	71327	F5N5	471729	49513	49515	SNP	1		C/T
63	AP001300	3	71327	F5N5	472185	55820	55822	SNP	1		C/A

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63	AP001300	3	71327	F5N5	472186	55893	55895	SNP	1		A/T
63	AP001300	3	71327	F5N5	472187	55395	55397	SNP	1		G/T
63	AP001300	3	71327	F5N5	472307	32224	32226	SNP	1		T/A
63	AP001300	3	71327	F5N5	472308	32233	32235	SNP	1		G/A
63	AP001300	3	71327	F5N5	472661	29749	29751	SNP	1		C/T
63	AP001300	3	71327	F5N5	473136	67200	67202	SNP	1		A/C
63	AP001300	3	71327	F5N5	473295	19703	19705	SNP	1		T/A
63	AP001300	3	71327	F5N5	473296	19702	19704	SNP	1		T/G
63	AP001300	3	71327	F5N5	473427	25411	25413	SNP	1		G/T
63	AP001300	3	71327	F5N5	473649	48237	48239	SNP	1		T/G
63	AP001300	3	71327	F5N5	473920	12970	14852	IND	2	1881/-1881	
63	AP001300	3	71327	F5N5	473921	1471	1472	IND	2	-6/6	
63	AP001300	3	71327	F5N5	473922	21246	21255	IND	2	8/-8	
63	AP001300	3	71327	F5N5	474261	15957	15958	IND	1	-1/1	
63	AP001300	3	71327	F5N5	474262	24094	24095	IND	1	-1/1	
63	AP001300	3	71327	F5N5	474263	55626	55627	IND	1	-1/1	
64	AP000733	3	2490	F28F4	472887	1752	1754	SNP	1		T/C
64	AP000733	3	2490	F28F4	472888	2136	2138	SNP	1		G/T
64	AP000733	3	2490	F28F4	473879	457	458	IND	2	-4/4	
64	AP000733	3	2490	F28F4	473880	458	459	IND	2	-4/4	
65	AB028621	3	78921	MUJ8	467302	61090	61092	SNP	1		A/T
65	AB028621	3	78921	MUJ8	467440	15246	15248	SNP	1		T/A
65	AB028621	3	78921	MUJ8	467441	15071	15073	SNP	1		A/C
65	AB028621	3	78921	MUJ8	467635	78664	78666	SNP	1		A/C
65	AB028621	3	78921	MUJ8	467687	27030	27032	SNP	1		T/A
65	AB028621	3	78921	MUJ8	467688	27029	27031	SNP	1		T/A
65	AB028621	3	78921	MUJ8	467799	33273	33275	SNP	1		C/T
65	AB028621	3	78921	MUJ8	468532	57374	57376	SNP	1		C/T
65	AB028621	3	78921	MUJ8	468581	76090	76092	SNP	1		A/T
65	AB028621	3	78921	MUJ8	468582	75837	75839	SNP	1		G/T
65	AB028621	3	78921	MUJ8	468600	63672	63674	SNP	1		A/T
65	AB028621	3	78921	MUJ8	468731	55687	55689	SNP	1		G/A
65	AB028621	3	78921	MUJ8	468732	55566	55568	SNP	1		G/A
65	AB028621	3	78921	MUJ8	468733	55671	55673	SNP	1		G/C
65	AB028621	3	78921	MUJ8	468734	55585	55587	SNP	1		T/C
65	AB028621	3	78921	MUJ8	468790	35409	35411	SNP	1		T/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
65	AB028621	3	78921	MUJ8	469082	41779	41781	SNP	1		T/G
65	AB028621	3	78921	MUJ8	469083	42935	42937	SNP	1		C/T
65	AB028621	3	78921	MUJ8	469107	45705	45707	SNP	1		T/C
65	AB028621	3	78921	MUJ8	469183	70603	70605	SNP	1		T/A
65	AB028621	3	78921	MUJ8	469184	71793	71795	SNP	1		A/C
65	AB028621	3	78921	MUJ8	469185	70593	70595	SNP	1		A/C
65	AB028621	3	78921	MUJ8	469186	70601	70603	SNP	1		G/C
65	AB028621	3	78921	MUJ8	469187	72069	72071	SNP	1		T/G
65	AB028621	3	78921	MUJ8	469188	72083	72085	SNP	1		T/G
65	AB028621	3	78921	MUJ8	469189	70604	70606	SNP	1		A/G
65	AB028621	3	78921	MUJ8	469190	71794	71796	SNP	1		A/T
65	AB028621	3	78921	MUJ8	469191	70594	70596	SNP	1		C/T
65	AB028621	3	78921	MUJ8	469323	16878	16880	SNP	1		A/G
65	AB028621	3	78921	MUJ8	470513	15927	15931	IND	2	3/-3	
65	AB028621	3	78921	MUJ8	470514	22565	22566	IND	2	-6/6	
65	AB028621	3	78921	MUJ8	470515	39450	39455	IND	2	4/-4	
65	AB028621	3	78921	MUJ8	470516	39506	39507	IND	2	-12/12	
65	AB028621	3	78921	MUJ8	470517	48592	48601	IND	2	8/-8	
65	AB028621	3	78921	MUJ8	470518	70603	70608	IND	2	4/-4	
65	AB028621	3	78921	MUJ8	470519	71128	71133	IND	2	4/-4	
65	AB028621	3	78921	MUJ8	470520	75229	75230	IND	2	-13/13	
65	AB028621	3	78921	MUJ8	471388	1196	1197	IND	1	-1/1	
65	AB028621	3	78921	MUJ8	471389	15929	15931	IND	1	1/-1	
65	AB028621	3	78921	MUJ8	471390	15932	15935	IND	1	2/-2	
65	AB028621	3	78921	MUJ8	471391	23747	23748	IND	1	-1/1	
65	AB028621	3	78921	MUJ8	471392	25686	25687	IND	1	-1/1	
65	AB028621	3	78921	MUJ8	471393	70596	70597	IND	1	-1/1	
65	AB028621	3	78921	MUJ8	471394	70599	70600	IND	1	-1/1	
65	AB028621	3	78921	MUJ8	471395	70606	70608	IND	1	1/-1	
65	AB028621	3	78921	MUJ8	471396	70696	70698	IND	1	1/-1	
65	AB028621	3	78921	MUJ8	471397	73274	73275	IND	1	-1/1	
66	AP000740	3	40018	MSD24	466917	34699	34701	SNP	1		G/C
66	AP000740	3	40018	MSD24	467637	38380	38382	SNP	1		T/C
66	AP000740	3	40018	MSD24	467638	38379	38381	SNP	1		A/T
66	AP000740	3	40018	MSD24	467639	39777	39779	SNP	1		G/A
66	AP000740	3	40018	MSD24	467640	39045	39047	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
66	AP000740	3	40018	MSD24	467641	39757	39759	SNP	1		A/G
66	AP000740	3	40018	MSD24	467840	15510	15512	SNP	1		T/G
66	AP000740	3	40018	MSD24	468363	35220	35222	SNP	1		T/C
66	AP000740	3	40018	MSD24	470509	22194	22206	IND	2	11/-11	
67	AB028609	3	78535	K7P8	471648	52758	52760	SNP	1		T/C
67	AB028609	3	78535	K7P8	471649	52843	52845	SNP	1		A/G
67	AB028609	3	78535	K7P8	471741	46997	46999	SNP	1		T/C
67	AB028609	3	78535	K7P8	471742	46659	46661	SNP	1		C/T
67	AB028609	3	78535	K7P8	471743	46641	46643	SNP	1		G/T
67	AB028609	3	78535	K7P8	471783	46153	46155	SNP	1		T/A
67	AB028609	3	78535	K7P8	471784	45789	45791	SNP	1		A/G
67	AB028609	3	78535	K7P8	471787	63370	63372	SNP	1		C/A
67	AB028609	3	78535	K7P8	471788	63440	63442	SNP	1		G/A
67	AB028609	3	78535	K7P8	471789	63400	63402	SNP	1		T/C
67	AB028609	3	78535	K7P8	471790	62842	62844	SNP	1		C/T
67	AB028609	3	78535	K7P8	471791	63442	63444	SNP	1		C/T
67	AB028609	3	78535	K7P8	471818	44801	44803	SNP	1		G/C
67	AB028609	3	78535	K7P8	471848	64918	64920	SNP	1		G/A
67	AB028609	3	78535	K7P8	471849	65568	65570	SNP	1		T/C
67	AB028609	3	78535	K7P8	471850	65582	65584	SNP	1		A/G
67	AB028609	3	78535	K7P8	471851	64923	64925	SNP	1		A/T
67	AB028609	3	78535	K7P8	471857	58818	58820	SNP	1		G/A
67	AB028609	3	78535	K7P8	471858	58849	58851	SNP	1		A/C
67	AB028609	3	78535	K7P8	471859	58900	58902	SNP	1		A/T
67	AB028609	3	78535	K7P8	471860	58355	58357	SNP	1		C/T
67	AB028609	3	78535	K7P8	471888	50018	50020	SNP	1		T/A
67	AB028609	3	78535	K7P8	471889	50132	50134	SNP	1		C/T
67	AB028609	3	78535	K7P8	471890	50110	50112	SNP	1		A/T
67	AB028609	3	78535	K7P8	471992	47776	47778	SNP	1		G/A
67	AB028609	3	78535	K7P8	471993	47725	47727	SNP	1		G/A
67	AB028609	3	78535	K7P8	471994	47731	47733	SNP	1		T/C
67	AB028609	3	78535	K7P8	471995	47703	47705	SNP	1		A/G
67	AB028609	3	78535	K7P8	471996	47734	47736	SNP	1		A/G
67	AB028609	3	78535	K7P8	471997	47680	47682	SNP	1		A/T
67	AB028609	3	78535	K7P8	472347	5275	5277	SNP	1		G/C
67	AB028609	3	78535	K7P8	472357	19647	19649	SNP	1		C/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
67	AB028609	3	78535	K7P8	472358	19648	19650	SNP	1		C/A
67	AB028609	3	78535	K7P8	472359	19856	19858	SNP	1		T/A
67	AB028609	3	78535	K7P8	472360	20067	20069	SNP	1		G/C
67	AB028609	3	78535	K7P8	472361	19924	19926	SNP	1		A/G
67	AB028609	3	78535	K7P8	472408	32586	32588	SNP	1		G/A
67	AB028609	3	78535	K7P8	472409	32707	32709	SNP	1		C/A
67	AB028609	3	78535	K7P8	472410	32404	32406	SNP	1		C/G
67	AB028609	3	78535	K7P8	472411	32405	32407	SNP	1		C/G
67	AB028609	3	78535	K7P8	472412	32391	32393	SNP	1		A/T
67	AB028609	3	78535	K7P8	472456	11607	11609	SNP	1		C/A
67	AB028609	3	78535	K7P8	472457	11205	11207	SNP	1		T/C
67	AB028609	3	78535	K7P8	472458	11313	11315	SNP	1		A/C
67	AB028609	3	78535	K7P8	472459	11349	11351	SNP	1		A/C
67	AB028609	3	78535	K7P8	472460	11354	11356	SNP	1		T/C
67	AB028609	3	78535	K7P8	472461	11401	11403	SNP	1		A/C
67	AB028609	3	78535	K7P8	472462	9962	9964	SNP	1		C/G
67	AB028609	3	78535	K7P8	472463	10288	10290	SNP	1		A/G
67	AB028609	3	78535	K7P8	472464	10529	10531	SNP	1		C/T
67	AB028609	3	78535	K7P8	472766	39419	39421	SNP	1		T/C
67	AB028609	3	78535	K7P8	472767	38763	38765	SNP	1		C/T
67	AB028609	3	78535	K7P8	472828	23787	23789	SNP	1		T/A
67	AB028609	3	78535	K7P8	472829	23788	23790	SNP	1		A/G
67	AB028609	3	78535	K7P8	472830	23789	23791	SNP	1		A/T
67	AB028609	3	78535	K7P8	473040	30590	30592	SNP	1		T/C
67	AB028609	3	78535	K7P8	473041	30476	30478	SNP	1		G/C
67	AB028609	3	78535	K7P8	473042	30304	30306	SNP	1		T/G
67	AB028609	3	78535	K7P8	473063	1820	1822	SNP	1		C/A
67	AB028609	3	78535	K7P8	473064	2096	2098	SNP	1		C/A
67	AB028609	3	78535	K7P8	473065	1979	1981	SNP	1		T/C
67	AB028609	3	78535	K7P8	473066	1899	1901	SNP	1		A/G
67	AB028609	3	78535	K7P8	473067	1695	1697	SNP	1		T/G
67	AB028609	3	78535	K7P8	473137	29138	29140	SNP	1		C/T
67	AB028609	3	78535	K7P8	473277	56867	56869	SNP	1		T/A
67	AB028609	3	78535	K7P8	473278	56945	56947	SNP	1		G/C
67	AB028609	3	78535	K7P8	473516	7436	7438	SNP	1		T/A
67	AB028609	3	78535	K7P8	473517	7449	7451	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
67	AB028609	3	78535	K7P8	473518	5912	5914	SNP	1		T/A
67	AB028609	3	78535	K7P8	473519	5783	5785	SNP	1		T/C
67	AB028609	3	78535	K7P8	473520	5794	5796	SNP	1		T/C
67	AB028609	3	78535	K7P8	473521	6443	6445	SNP	1		A/C
67	AB028609	3	78535	K7P8	473522	7245	7247	SNP	1		T/G
67	AB028609	3	78535	K7P8	473523	6447	6449	SNP	1		C/T
67	AB028609	3	78535	K7P8	473942	11489	11497	IND	2	7/-7	
67	AB028609	3	78535	K7P8	473943	15247	15251	IND	2	3/-3	
67	AB028609	3	78535	K7P8	473944	17673	17674	IND	2	-20/20	
67	AB028609	3	78535	K7P8	473945	17784	17785	IND	2	-4/4	
67	AB028609	3	78535	K7P8	473946	18955	18956	IND	2	-4/4	
67	AB028609	3	78535	K7P8	473947	24570	24577	IND	2	6/-6	
67	AB028609	3	78535	K7P8	473948	4407	4408	IND	2	-3/3	
67	AB028609	3	78535	K7P8	474326	11489	11494	IND	1	4/-4	
67	AB028609	3	78535	K7P8	474327	11494	11498	IND	1	3/-3	
67	AB028609	3	78535	K7P8	474328	20205	20206	IND	1	-1/1	
67	AB028609	3	78535	K7P8	474329	30383	30384	IND	1	-1/1	
67	AB028609	3	78535	K7P8	474330	32396	32398	IND	1	1/-1	
67	AB028609	3	78535	K7P8	474331	32401	32403	IND	1	1/-1	
67	AB028609	3	78535	K7P8	474332	38616	38617	IND	1	-2/2	
67	AB028609	3	78535	K7P8	474333	38751	38752	IND	1	-1/1	
67	AB028609	3	78535	K7P8	474334	4422	4423	IND	1	-3/3	
67	AB028609	3	78535	K7P8	474335	44747	44748	IND	1	-2/2	
67	AB028609	3	78535	K7P8	474336	59400	59404	IND	1	3/-3	
67	AB028609	3	78535	K7P8	474337	59404	59408	IND	1	3/-3	
67	AB028609	3	78535	K7P8	474338	6196	6198	IND	1	1/-1	
67	AB028609	3	78535	K7P8	474339	63104	63106	IND	1	1/-1	
68	AB028607	3	77483	K13N2	471687	41581	41583	SNP	1		T/C
68	AB028607	3	77483	K13N2	471807	35573	35575	SNP	1		C/T
68	AB028607	3	77483	K13N2	472380	59690	59692	SNP	1		T/C
68	AB028607	3	77483	K13N2	472381	59706	59708	SNP	1		G/T
68	AB028607	3	77483	K13N2	472382	59514	59516	SNP	1		G/T
68	AB028607	3	77483	K13N2	472407	47769	47771	SNP	1		C/T
68	AB028607	3	77483	K13N2	472629	72454	72456	SNP	1		T/A
68	AB028607	3	77483	K13N2	472630	72688	72690	SNP	1		G/C
68	AB028607	3	77483	K13N2	472631	72608	72610	SNP	1		A/G

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68	AB028607	3	77483	K13N2	472632	72442	72444	SNP	1		A/T
68	AB028607	3	77483	K13N2	472633	72541	72543	SNP	1		C/T
68	AB028607	3	77483	K13N2	472634	72672	72674	SNP	1		C/T
68	AB028607	3	77483	K13N2	472801	28928	28930	SNP	1		T/A
68	AB028607	3	77483	K13N2	472802	28945	28947	SNP	1		A/G
68	AB028607	3	77483	K13N2	472803	28982	28984	SNP	1		C/T
68	AB028607	3	77483	K13N2	473932	10370	10371	IND	2	-6/6	
68	AB028607	3	77483	K13N2	473933	12416	12417	IND	2	-3/3	
68	AB028607	3	77483	K13N2	473934	14527	14544	IND	2	16/-16	
68	AB028607	3	77483	K13N2	474311	35555	35556	IND	1	-1/1	
69	AP001298	3	71184	F20C19	471703	4653	4655	SNP	1		A/T
69	AP001298	3	71184	F20C19	471777	5147	5149	SNP	1		C/T
69	AP001298	3	71184	F20C19	471778	4946	4948	SNP	1		C/T
69	AP001298	3	71184	F20C19	471926	58697	58699	SNP	1		G/A
69	AP001298	3	71184	F20C19	471927	58393	58395	SNP	1		T/C
69	AP001298	3	71184	F20C19	472019	13441	13443	SNP	1		G/A
69	AP001298	3	71184	F20C19	472020	13393	13395	SNP	1		C/G
69	AP001298	3	71184	F20C19	472021	13377	13379	SNP	1		A/G
69	AP001298	3	71184	F20C19	472022	13560	13562	SNP	1		A/T
69	AP001298	3	71184	F20C19	472572	50704	50706	SNP	1		C/G
69	AP001298	3	71184	F20C19	472757	68471	68473	SNP	1		C/G
69	AP001298	3	71184	F20C19	472812	54115	54117	SNP	1		G/A
69	AP001298	3	71184	F20C19	472813	53841	53843	SNP	1		C/G
69	AP001298	3	71184	F20C19	472814	54111	54113	SNP	1		T/G
69	AP001298	3	71184	F20C19	472831	30260	30262	SNP	1		T/C
69	AP001298	3	71184	F20C19	472832	30321	30323	SNP	1		A/T
69	AP001298	3	71184	F20C19	472905	43596	43598	SNP	1		G/A
69	AP001298	3	71184	F20C19	472906	43518	43520	SNP	1		G/A
69	AP001298	3	71184	F20C19	472982	62299	62301	SNP	1		C/G
69	AP001298	3	71184	F20C19	473068	70734	70736	SNP	1		T/C
69	AP001298	3	71184	F20C19	473108	27356	27358	SNP	1		A/C
69	AP001298	3	71184	F20C19	473490	19773	19775	SNP	1		T/A
69	AP001298	3	71184	F20C19	473491	20045	20047	SNP	1		A/G
69	AP001298	3	71184	F20C19	473629	52762	52764	SNP	1		T/C
69	AP001298	3	71184	F20C19	473630	52757	52759	SNP	1		G/C
69	AP001298	3	71184	F20C19	473631	52575	52577	SNP	1		G/C

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69	AP001298	3	71184	F20C19	473632	52444	52446	SNP	1		T/C
69	AP001298	3	71184	F20C19	473633	52403	52405	SNP	1		A/C
69	AP001298	3	71184	F20C19	473634	52710	52712	SNP	1		A/G
69	AP001298	3	71184	F20C19	473635	52690	52692	SNP	1		C/T
69	AP001298	3	71184	F20C19	473636	52680	52682	SNP	1		A/T
69	AP001298	3	71184	F20C19	473854	6172	6211	IND	2	38/-38	
69	AP001298	3	71184	F20C19	474104	16827	16828	IND	1	-1/1	
69	AP001298	3	71184	F20C19	474105	41066	41067	IND	1	-1/1	
69	AP001298	3	71184	F20C19	474106	50769	50771	IND	1	1/-1	
70	AB028611	3	82646	MFE16	466957	80355	80357	SNP	1		A/G
70	AB028611	3	82646	MFE16	466958	80295	80297	SNP	1		C/T
70	AB028611	3	82646	MFE16	466959	79918	79920	SNP	1		C/T
70	AB028611	3	82646	MFE16	466976	15118	15120	SNP	1		T/A
70	AB028611	3	82646	MFE16	466977	15555	15557	SNP	1		G/A
70	AB028611	3	82646	MFE16	466978	15058	15060	SNP	1		C/T
70	AB028611	3	82646	MFE16	467322	65826	65828	SNP	1		T/A
70	AB028611	3	82646	MFE16	467323	65611	65613	SNP	1		A/G
70	AB028611	3	82646	MFE16	467324	65713	65715	SNP	1		C/T
70	AB028611	3	82646	MFE16	468085	75232	75234	SNP	1		T/C
70	AB028611	3	82646	MFE16	468086	75505	75507	SNP	1		A/T
70	AB028611	3	82646	MFE16	468778	3956	3958	SNP	1		G/A
70	AB028611	3	82646	MFE16	468779	3891	3893	SNP	1		C/T
70	AB028611	3	82646	MFE16	469262	39561	39563	SNP	1		G/A
70	AB028611	3	82646	MFE16	469263	39816	39818	SNP	1		G/C
70	AB028611	3	82646	MFE16	470407	10092	10103	IND	2	10/-10	
70	AB028611	3	82646	MFE16	470408	14365	14366	IND	2	-3/3	
70	AB028611	3	82646	MFE16	470409	16468	28746	IND	2	12277/-12277	
70	AB028611	3	82646	MFE16	470410	27131	27161	IND	2	29/-29	
70	AB028611	3	82646	MFE16	470411	27132	27162	IND	2	29/-29	
70	AB028611	3	82646	MFE16	470412	28822	28830	IND	2	7/-7	
70	AB028611	3	82646	MFE16	470413	31985	33179	IND	2	1193/-1193	
70	AB028611	3	82646	MFE16	470414	348	360	IND	2	11/-11	
70	AB028611	3	82646	MFE16	470415	36049	36050	IND	2	-10/10	
70	AB028611	3	82646	MFE16	470416	367	379	IND	2	11/-11	
70	AB028611	3	82646	MFE16	470417	4453	4454	IND	2	-3/3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
70	AB028611	3	82646	MFE16	470418	61630	61638	IND	2	7/-7	
70	AB028611	3	82646	MFE16	470419	63513	63523	IND	2	9/-9	
70	AB028611	3	82646	MFE16	470420	71755	71764	IND	2	8/-8	
70	AB028611	3	82646	MFE16	470421	727	744	IND	2	16/-16	
70	AB028611	3	82646	MFE16	470422	728	745	IND	2	16/-16	
70	AB028611	3	82646	MFE16	470423	74046	74052	IND	2	5/-5	
70	AB028611	3	82646	MFE16	470424	77821	77822	IND	2	-15/15	
70	AB028611	3	82646	MFE16	470425	77824	77825	IND	2	-15/15	
70	AB028611	3	82646	MFE16	470426	78953	78966	IND	2	12/-12	
70	AB028611	3	82646	MFE16	470427	79710	79711	IND	2	-9/9	
70	AB028611	3	82646	MFE16	471382	75265	75267	IND	1	1/-1	
70	AB028611	3	82646	MFE16	471383	75333	75335	IND	1	1/-1	
71	AB028616	3	86139	MMG15	467396	38749	38751	SNP	1		T/A
71	AB028616	3	86139	MMG15	467397	38896	38898	SNP	1		T/A
71	AB028616	3	86139	MMG15	467398	38281	38283	SNP	1		T/C
71	AB028616	3	86139	MMG15	467399	38248	38250	SNP	1		C/G
71	AB028616	3	86139	MMG15	468108	66535	66537	SNP	1		C/A
71	AB028616	3	86139	MMG15	468781	27368	27370	SNP	1		T/C
71	AB028616	3	86139	MMG15	468813	16568	16570	SNP	1		A/G
71	AB028616	3	86139	MMG15	469135	31665	31667	SNP	1		A/G
71	AB028616	3	86139	MMG15	470465	19388	19389	IND	2	-9/9	
71	AB028616	3	86139	MMG15	470466	31872	31892	IND	2	19/-19	
71	AB028616	3	86139	MMG15	470467	47865	47878	IND	2	12/-12	
71	AB028616	3	86139	MMG15	470468	56619	56620	IND	2	-6/6	
71	AB028616	3	86139	MMG15	470469	68665	68670	IND	2	4/-4	
71	AB028616	3	86139	MMG15	470470	73388	73392	IND	2	3/-3	
71	AB028616	3	86139	MMG15	470471	73831	73836	IND	2	4/-4	
71	AB028616	3	86139	MMG15	470472	73968	73977	IND	2	8/-8	
72	AB028618	3	85690	MOD1	467605	78264	78266	SNP	1		A/T
72	AB028618	3	85690	MOD1	468067	60214	60216	SNP	1		A/C
72	AB028618	3	85690	MOD1	468068	60328	60330	SNP	1		A/G
72	AB028618	3	85690	MOD1	468072	21474	21476	SNP	1		A/G
72	AB028618	3	85690	MOD1	468073	21277	21279	SNP	1		A/T
72	AB028618	3	85690	MOD1	468784	64847	64849	SNP	1		A/G
72	AB028618	3	85690	MOD1	468785	64276	64278	SNP	1		C/G
72	AB028618	3	85690	MOD1	468786	64219	64221	SNP	1		T/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
72	AB028618	3	85690	MOD1	470488	12858	12859	IND	2	-7/7	
72	AB028618	3	85690	MOD1	470489	1447	1452	IND	2	4/-4	
72	AB028618	3	85690	MOD1	470490	34068	34069	IND	2	-10/10	
72	AB028618	3	85690	MOD1	470491	36068	36175	IND	2	106/-106	
72	AB028618	3	85690	MOD1	470492	43345	43346	IND	2	-10/10	
72	AB028618	3	85690	MOD1	470493	51860	52023	IND	2	162/-162	
72	AB028618	3	85690	MOD1	470494	66731	66853	IND	2	121/-121	
72	AB028618	3	85690	MOD1	470495	73641	73646	IND	2	4/-4	
72	AB028618	3	85690	MOD1	470496	80819	80872	IND	2	52/-52	
72	AB028618	3	85690	MOD1	470497	82758	82811	IND	2	52/-52	
72	AB028618	3	85690	MOD1	470498	84696	84749	IND	2	52/-52	
72	AB028618	3	85690	MOD1	470499	949	9097	IND	2	8147/-8147	
73	AP000736	3	82356	K17E7	471646	72686	72688	SNP	1		T/G
73	AP000736	3	82356	K17E7	471647	72662	72664	SNP	1		C/G
73	AP000736	3	82356	K17E7	471745	76862	76864	SNP	1		G/C
73	AP000736	3	82356	K17E7	471836	1268	1270	SNP	1		T/G
73	AP000736	3	82356	K17E7	471862	7689	7691	SNP	1		G/A
73	AP000736	3	82356	K17E7	471863	7747	7749	SNP	1		C/T
73	AP000736	3	82356	K17E7	471952	34965	34967	SNP	1		G/A
73	AP000736	3	82356	K17E7	471953	34984	34986	SNP	1		A/C
73	AP000736	3	82356	K17E7	471954	34956	34958	SNP	1		A/C
73	AP000736	3	82356	K17E7	471955	35096	35098	SNP	1		T/G
73	AP000736	3	82356	K17E7	471956	205	207	SNP	1		A/G
73	AP000736	3	82356	K17E7	472016	75563	75565	SNP	1		G/C
73	AP000736	3	82356	K17E7	472017	75703	75705	SNP	1		G/T
73	AP000736	3	82356	K17E7	472277	38174	38176	SNP	1		C/A
73	AP000736	3	82356	K17E7	472278	38273	38275	SNP	1		A/C
73	AP000736	3	82356	K17E7	472279	38203	38205	SNP	1		T/G
73	AP000736	3	82356	K17E7	472280	38279	38281	SNP	1		C/G
73	AP000736	3	82356	K17E7	472653	48716	48718	SNP	1		T/A
73	AP000736	3	82356	K17E7	472654	48603	48605	SNP	1		T/G
73	AP000736	3	82356	K17E7	472655	48308	48310	SNP	1		A/T
73	AP000736	3	82356	K17E7	473935	2314	2390	IND	2	75/-75	
73	AP000736	3	82356	K17E7	473936	2317	2393	IND	2	75/-75	
73	AP000736	3	82356	K17E7	473937	9598	9599	IND	2	-23/23	
73	AP000736	3	82356	K17E7	474312	48313	48314	IND	1	-1/1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
73	AP000736	3	82356	K17E7	474313	48372	48374	IND	1	1/-1	
74	AB028615	3	84157	MIL15	467375	17323	17325	SNP	1		A/C
74	AB028615	3	84157	MIL15	467376	17019	17021	SNP	1		G/C
74	AB028615	3	84157	MIL15	470439	10218	10222	IND	2	3/-3	
74	AB028615	3	84157	MIL15	470440	13002	13011	IND	2	8/-8	
74	AB028615	3	84157	MIL15	470441	62234	63377	IND	2	1142/-1142	
74	AB028615	3	84157	MIL15	470442	6308	6319	IND	2	10/-10	
74	AB028615	3	84157	MIL15	470443	6494	6502	IND	2	7/-7	
74	AB028615	3	84157	MIL15	470444	65796	65805	IND	2	8/-8	
74	AB028615	3	84157	MIL15	470445	65859	65872	IND	2	12/-12	
74	AB028615	3	84157	MIL15	470446	65911	65912	IND	2	-4/4	
74	AB028615	3	84157	MIL15	470447	66102	66125	IND	2	22/-22	
74	AB028615	3	84157	MIL15	470448	77850	77854	IND	2	3/-3	
74	AB028615	3	84157	MIL15	470449	77984	77985	IND	2	-4/4	
74	AB028615	3	84157	MIL15	470450	81954	81960	IND	2	5/-5	
74	AB028615	3	84157	MIL15	470451	82097	82102	IND	2	4/-4	
75	AP000732	3	64714	F21A17	471770	5116	5118	SNP	1		C/A
75	AP000732	3	64714	F21A17	471771	5493	5495	SNP	1		G/A
75	AP000732	3	64714	F21A17	471772	5743	5745	SNP	1		T/G
75	AP000732	3	64714	F21A17	471773	5655	5657	SNP	1		A/G
75	AP000732	3	64714	F21A17	471774	5274	5276	SNP	1		C/T
75	AP000732	3	64714	F21A17	471775	5470	5472	SNP	1		C/T
75	AP000732	3	64714	F21A17	471776	5617	5619	SNP	1		C/T
75	AP000732	3	64714	F21A17	473855	366	379	IND	2	12/-12	
75	AP000732	3	64714	F21A17	474107	4930	4931	IND	1	-1/1	
75	AP000732	3	64714	F21A17	474108	5044	5047	IND	1	2/-2	
75	AP000732	3	64714	F21A17	474109	5510	5513	IND	1	2/-2	
76	AB028614	3	82347	MIF6	470437	4626	5492	IND	2	865/-865	
76	AB028614	3	82347	MIF6	470438	78167	78180	IND	2	12/-12	
77	AL138652	3	91567	T18B22	472211	81168	81170	SNP	1		T/C
77	AL138652	3	91567	T18B22	472212	81114	81116	SNP	1		T/C
77	AL138652	3	91567	T18B22	472213	81117	81119	SNP	1		C/G
77	AL138652	3	91567	T18B22	472214	80706	80708	SNP	1		G/T
77	AL138652	3	91567	T18B22	472215	81166	81168	SNP	1		C/T
77	AL138652	3	91567	T18B22	474407	80698	80699	IND	1	-1/1	
78	AL138649	3	88010	T14D3	471827	15133	15135	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
78	AL138649	3	88010	T14D3	471828	15087	15089	SNP	1		T/G
78	AL138649	3	88010	T14D3	471829	14980	14982	SNP	1		C/G
78	AL138649	3	88010	T14D3	472160	44676	44678	SNP	1		C/T
78	AL138649	3	88010	T14D3	472304	28613	28615	SNP	1		G/A
78	AL138649	3	88010	T14D3	472305	28953	28955	SNP	1		A/C
78	AL138649	3	88010	T14D3	472306	28936	28938	SNP	1		A/T
78	AL138649	3	88010	T14D3	472378	69969	69971	SNP	1		G/A
78	AL138649	3	88010	T14D3	472379	70223	70225	SNP	1		A/T
78	AL138649	3	88010	T14D3	472392	64461	64463	SNP	1		G/A
78	AL138649	3	88010	T14D3	472393	64449	64451	SNP	1		G/C
78	AL138649	3	88010	T14D3	472394	64302	64304	SNP	1		G/C
78	AL138649	3	88010	T14D3	472395	64341	64343	SNP	1		A/G
78	AL138649	3	88010	T14D3	472396	64475	64477	SNP	1		C/T
78	AL138649	3	88010	T14D3	472489	85093	85095	SNP	1		G/A
78	AL138649	3	88010	T14D3	472490	85272	85274	SNP	1		G/A
78	AL138649	3	88010	T14D3	472491	85094	85096	SNP	1		T/C
78	AL138649	3	88010	T14D3	472492	84953	84955	SNP	1		C/T
78	AL138649	3	88010	T14D3	472676	40020	40022	SNP	1		C/T
78	AL138649	3	88010	T14D3	472889	42496	42498	SNP	1		A/G
78	AL138649	3	88010	T14D3	472890	42497	42499	SNP	1		A/G
78	AL138649	3	88010	T14D3	472891	41978	41980	SNP	1		A/G
78	AL138649	3	88010	T14D3	472926	60235	60237	SNP	1		T/C
78	AL138649	3	88010	T14D3	472992	49968	49970	SNP	1		G/A
78	AL138649	3	88010	T14D3	472993	50016	50018	SNP	1		G/C
78	AL138649	3	88010	T14D3	472994	49835	49837	SNP	1		A/G
78	AL138649	3	88010	T14D3	472995	50064	50066	SNP	1		A/G
78	AL138649	3	88010	T14D3	473493	81373	81375	SNP	1		G/C
78	AL138649	3	88010	T14D3	473494	81295	81297	SNP	1		A/T
78	AL138649	3	88010	T14D3	473495	81297	81299	SNP	1		A/T
78	AL138649	3	88010	T14D3	473535	61931	61933	SNP	1		T/A
78	AL138649	3	88010	T14D3	473536	61896	61898	SNP	1		A/C
78	AL138649	3	88010	T14D3	473537	61874	61876	SNP	1		G/T
78	AL138649	3	88010	T14D3	473542	80330	80332	SNP	1		G/A
78	AL138649	3	88010	T14D3	473543	79731	79733	SNP	1		A/G
78	AL138649	3	88010	T14D3	473681	12147	12149	SNP	1		T/A
78	AL138649	3	88010	T14D3	473682	12157	12159	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
78	AL138649	3	88010	T14D3	473683	12158	12160	SNP	1		T/A
78	AL138649	3	88010	T14D3	473684	12151	12153	SNP	1		A/T
78	AL138649	3	88010	T14D3	473685	12152	12154	SNP	1		A/T
78	AL138649	3	88010	T14D3	473686	12153	12155	SNP	1		A/T
78	AL138649	3	88010	T14D3	473715	30965	30967	SNP	1		C/G
78	AL138649	3	88010	T14D3	473716	30502	30504	SNP	1		T/G
78	AL138649	3	88010	T14D3	474375	12154	12156	IND	1	1/-1	
78	AL138649	3	88010	T14D3	474376	28845	28846	IND	1	-1/1	
78	AL138649	3	88010	T14D3	474377	30947	30948	IND	1	-1/1	
78	AL138649	3	88010	T14D3	474378	49830	49832	IND	1	1/-1	
78	AL138649	3	88010	T14D3	474379	50136	50138	IND	1	1/-1	
78	AL138649	3	88010	T14D3	474380	81376	81377	IND	1	-1/1	
78	AL138649	3	88010	T14D3	474381	84995	84997	IND	1	1/-1	
79	AL132953	3	91274	F18N11	467042	49849	49851	SNP	1		G/A
79	AL132953	3	91274	F18N11	467388	974	976	SNP	1		G/A
79	AL132953	3	91274	F18N11	467389	1153	1155	SNP	1		G/A
79	AL132953	3	91274	F18N11	467390	975	977	SNP	1		T/C
79	AL132953	3	91274	F18N11	467391	834	836	SNP	1		C/T
79	AL132953	3	91274	F18N11	468103	34457	34459	SNP	1		T/A
79	AL132953	3	91274	F18N11	468104	34317	34319	SNP	1		G/A
79	AL132953	3	91274	F18N11	468105	34492	34494	SNP	1		A/G
79	AL132953	3	91274	F18N11	468106	34424	34426	SNP	1		C/T
79	AL132953	3	91274	F18N11	468107	35061	35063	SNP	1		C/T
79	AL132953	3	91274	F18N11	468334	33071	33073	SNP	1		T/G
79	AL132953	3	91274	F18N11	469279	38976	38978	SNP	1		G/A
79	AL132953	3	91274	F18N11	469280	39204	39206	SNP	1		A/T
79	AL132953	3	91274	F18N11	469768	13015	13016	IND	2	-3/3	
79	AL132953	3	91274	F18N11	469769	13160	13161	IND	2	-11/11	
79	AL132953	3	91274	F18N11	469770	19558	19559	IND	2	-6/6	
79	AL132953	3	91274	F18N11	469771	25307	25308	IND	2	-7/7	
79	AL132953	3	91274	F18N11	469772	25318	25319	IND	2	-7/7	
79	AL132953	3	91274	F18N11	469773	46586	46600	IND	2	13/-13	
79	AL132953	3	91274	F18N11	469774	47279	47286	IND	2	6/-6	
79	AL132953	3	91274	F18N11	469775	47338	47339	IND	2	-6/6	
79	AL132953	3	91274	F18N11	469776	47389	47390	IND	2	-10/10	
79	AL132953	3	91274	F18N11	469777	48396	48397	IND	2	-10/10	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
79	AL132953	3	91274	F18N11	469778	48524	48525	IND	2	-3/3	
79	AL132953	3	91274	F18N11	469779	49101	49102	IND	2	-3/3	
79	AL132953	3	91274	F18N11	469780	72197	72221	IND	2	23/-23	
79	AL132953	3	91274	F18N11	469781	75760	75761	IND	2	-15/15	
79	AL132953	3	91274	F18N11	469782	76040	76045	IND	2	4/-4	
79	AL132953	3	91274	F18N11	469783	78097	78098	IND	2	-7/7	
79	AL132953	3	91274	F18N11	469784	84176	84186	IND	2	9/-9	
79	AL132953	3	91274	F18N11	469785	89930	89931	IND	2	-4/4	
79	AL132953	3	91274	F18N11	469786	89931	89932	IND	2	-4/4	
79	AL132953	3	91274	F18N11	469787	90232	90236	IND	2	3/-3	
79	AL132953	3	91274	F18N11	471186	33021	33022	IND	1	-1/1	
79	AL132953	3	91274	F18N11	471187	876	878	IND	1	1/-1	
80	AL138657	3	110980	F9K21	471877	3729	3731	SNP	1		G/A
80	AL138657	3	110980	F9K21	471878	3694	3696	SNP	1		T/A
80	AL138657	3	110980	F9K21	471879	3685	3687	SNP	1		G/A
80	AL138657	3	110980	F9K21	471880	3661	3663	SNP	1		G/A
80	AL138657	3	110980	F9K21	471881	3634	3636	SNP	1		C/A
80	AL138657	3	110980	F9K21	471882	3766	3768	SNP	1		T/C
80	AL138657	3	110980	F9K21	471883	3705	3707	SNP	1		T/C
80	AL138657	3	110980	F9K21	471884	3688	3690	SNP	1		A/C
80	AL138657	3	110980	F9K21	471885	3679	3681	SNP	1		A/C
80	AL138657	3	110980	F9K21	471886	3646	3648	SNP	1		A/G
80	AL138657	3	110980	F9K21	471887	3907	3909	SNP	1		A/G
80	AL138657	3	110980	F9K21	472094	18205	18207	SNP	1		G/A
80	AL138657	3	110980	F9K21	472095	18465	18467	SNP	1		G/C
80	AL138657	3	110980	F9K21	473798	74940	74942	SNP	1		A/G
80	AL138657	3	110980	F9K21	473799	75084	75086	SNP	1		C/T
80	AL138657	3	110980	F9K21	474301	18388	18389	IND	1	-1/1	
81	AL133298	3	100328	F18L15	468139	79441	79443	SNP	1		T/A
81	AL133298	3	100328	F18L15	468140	79557	79559	SNP	1		G/C
81	AL133298	3	100328	F18L15	468141	79613	79615	SNP	1		A/C
81	AL133298	3	100328	F18L15	468142	79453	79455	SNP	1		A/G
81	AL133298	3	100328	F18L15	468143	79509	79511	SNP	1		A/G
81	AL133298	3	100328	F18L15	469761	11608	11609	IND	2	-5/5	
81	AL133298	3	100328	F18L15	469762	73195	73600	IND	2	404/-404	
81	AL133298	3	100328	F18L15	469763	97560	97564	IND	2	3/-3	

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81	AL133298	3	100328	F18L15	469764	97824	97855	IND	2	30/-30	
81	AL133298	3	100328	F18L15	469765	98247	98553	IND	2	305/-305	
81	AL133298	3	100328	F18L15	469766	99104	99105	IND	2	-4/4	
81	AL133298	3	100328	F18L15	469767	99149	99150	IND	2	-5/5	
81	AL133298	3	100328	F18L15	471185	88382	88384	IND	1	1/-1	
82	AL133314	3	100815	F12A12	467656	36392	36394	SNP	1		G/A
82	AL133314	3	100815	F12A12	468057	61999	62001	SNP	1		C/A
82	AL133314	3	100815	F12A12	468058	62148	62150	SNP	1		G/A
82	AL133314	3	100815	F12A12	468059	62251	62253	SNP	1		T/A
82	AL133314	3	100815	F12A12	468060	60589	60591	SNP	1		G/A
82	AL133314	3	100815	F12A12	468061	62255	62257	SNP	1		T/C
82	AL133314	3	100815	F12A12	468062	62027	62029	SNP	1		G/T
82	AL133314	3	100815	F12A12	468063	62260	62262	SNP	1		C/T
82	AL133314	3	100815	F12A12	468216	65706	65708	SNP	1		T/A
82	AL133314	3	100815	F12A12	468217	65476	65478	SNP	1		G/T
82	AL133314	3	100815	F12A12	468218	65484	65486	SNP	1		C/T
82	AL133314	3	100815	F12A12	468296	25667	25669	SNP	1		T/A
82	AL133314	3	100815	F12A12	468297	25654	25656	SNP	1		C/T
82	AL133314	3	100815	F12A12	468298	25691	25693	SNP	1		C/T
82	AL133314	3	100815	F12A12	468903	91001	91003	SNP	1		T/G
82	AL133314	3	100815	F12A12	469145	26405	26407	SNP	1		T/A
82	AL133314	3	100815	F12A12	469146	26406	26408	SNP	1		T/A
82	AL133314	3	100815	F12A12	469307	37556	37558	SNP	1		T/A
82	AL133314	3	100815	F12A12	469308	37548	37550	SNP	1		T/A
82	AL133314	3	100815	F12A12	469309	38418	38420	SNP	1		C/T
82	AL133314	3	100815	F12A12	469476	59415	59417	SNP	1		A/G
82	AL133314	3	100815	F12A12	469542	10476	10480	IND	2	3/-3	
82	AL133314	3	100815	F12A12	469543	11163	11469	IND	2	305/-305	
82	AL133314	3	100815	F12A12	469544	12020	12021	IND	2	-4/4	
82	AL133314	3	100815	F12A12	469545	12065	12066	IND	2	-5/5	
82	AL133314	3	100815	F12A12	469546	13231	13232	IND	2	-21/21	
82	AL133314	3	100815	F12A12	469547	13233	13234	IND	2	-21/21	
82	AL133314	3	100815	F12A12	469548	13704	13717	IND	2	12/-12	
82	AL133314	3	100815	F12A12	469549	21555	21556	IND	2	-4/4	
82	AL133314	3	100815	F12A12	469550	21699	21703	IND	2	3/-3	
82	AL133314	3	100815	F12A12	469551	21719	22527	IND	2	807/-807	

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82	AL133314	3	100815	F12A12	469552	22608	22621	IND	2	12/-12	
82	AL133314	3	100815	F12A12	469553	22881	22882	IND	2	-3/3	
82	AL133314	3	100815	F12A12	469554	65751	65752	IND	2	-3/3	
82	AL133314	3	100815	F12A12	469555	73379	73380	IND	2	-12/12	
82	AL133314	3	100815	F12A12	469556	74878	74891	IND	2	12/-12	
82	AL133314	3	100815	F12A12	469557	75008	75009	IND	2	-6/6	
82	AL133314	3	100815	F12A12	469558	76923	76933	IND	2	9/-9	
82	AL133314	3	100815	F12A12	469559	83191	83192	IND	2	-3/3	
82	AL133314	3	100815	F12A12	469560	98921	98928	IND	2	6/-6	
82	AL133314	3	100815	F12A12	469561	99041	99046	IND	2	4/-4	
82	AL133314	3	100815	F12A12	471090	25823	25824	IND	1	-1/1	
82	AL133314	3	100815	F12A12	471091	25824	25825	IND	1	-1/1	
82	AL133314	3	100815	F12A12	471092	38421	38422	IND	1	-2/2	
82	AL133314	3	100815	F12A12	471093	61741	61742	IND	1	-1/1	
82	AL133314	3	100815	F12A12	471094	62184	62185	IND	1	-1/1	
82	AL133314	3	100815	F12A12	471095	65581	65582	IND	1	-1/1	
83	AL133292	3	140680	F13I12	467076	63613	63615	SNP	1		G/T
83	AL133292	3	140680	F13I12	467319	64941	64943	SNP	1		G/C
83	AL133292	3	140680	F13I12	467320	65435	65437	SNP	1		C/T
83	AL133292	3	140680	F13I12	467321	64857	64859	SNP	1		A/T
83	AL133292	3	140680	F13I12	467385	50870	50872	SNP	1		G/A
83	AL133292	3	140680	F13I12	467386	50803	50805	SNP	1		C/G
83	AL133292	3	140680	F13I12	467387	115574	115576	SNP	1		A/G
83	AL133292	3	140680	F13I12	467985	38211	38213	SNP	1		A/G
83	AL133292	3	140680	F13I12	468877	29720	29722	SNP	1		A/C
83	AL133292	3	140680	F13I12	468878	29664	29666	SNP	1		A/G
83	AL133292	3	140680	F13I12	469027	48694	48696	SNP	1		T/A
83	AL133292	3	140680	F13I12	469028	48727	48729	SNP	1		A/T
83	AL133292	3	140680	F13I12	469029	42913	42915	SNP	1		C/A
83	AL133292	3	140680	F13I12	469030	42903	42905	SNP	1		G/A
83	AL133292	3	140680	F13I12	469031	42316	42318	SNP	1		T/C
83	AL133292	3	140680	F13I12	469032	42371	42373	SNP	1		T/G
83	AL133292	3	140680	F13I12	469033	42319	42321	SNP	1		C/T
83	AL133292	3	140680	F13I12	469034	42926	42928	SNP	1		C/T
83	AL133292	3	140680	F13I12	469256	104099	104101	SNP	1		C/A
83	AL133292	3	140680	F13I12	469257	104171	104173	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
83	AL133292	3	140680	F13I12	469258	104168	104170	SNP	1		A/G
83	AL133292	3	140680	F13I12	469467	27490	27492	SNP	1		T/C
83	AL133292	3	140680	F13I12	469592	107040	107053	IND	2	12/-12	
83	AL133292	3	140680	F13I12	469593	107093	107097	IND	2	3/-3	
83	AL133292	3	140680	F13I12	469594	109104	109105	IND	2	-8/8	
83	AL133292	3	140680	F13I12	469595	11459	11478	IND	2	18/-18	
83	AL133292	3	140680	F13I12	469596	11495	11496	IND	2	-9/9	
83	AL133292	3	140680	F13I12	469597	127760	128221	IND	2	460/-460	
83	AL133292	3	140680	F13I12	469598	13739	13752	IND	2	12/-12	
83	AL133292	3	140680	F13I12	469599	13796	13797	IND	2	-14/14	
83	AL133292	3	140680	F13I12	469600	16578	18706	IND	2	2127/-2127	
83	AL133292	3	140680	F13I12	469601	29667	29668	IND	2	-12/12	
83	AL133292	3	140680	F13I12	469602	47339	47343	IND	2	3/-3	
83	AL133292	3	140680	F13I12	469603	57432	57439	IND	2	6/-6	
83	AL133292	3	140680	F13I12	469604	57830	57834	IND	2	3/-3	
83	AL133292	3	140680	F13I12	469605	58714	58741	IND	2	26/-26	
83	AL133292	3	140680	F13I12	469606	77616	77631	IND	2	14/-14	
83	AL133292	3	140680	F13I12	469607	80498	80499	IND	2	-8/8	
83	AL133292	3	140680	F13I12	469608	81265	81266	IND	2	-3/3	
83	AL133292	3	140680	F13I12	469609	82044	82059	IND	2	14/-14	
83	AL133292	3	140680	F13I12	471113	115562	115563	IND	1	-1/1	
83	AL133292	3	140680	F13I12	471114	27483	27485	IND	1	1/-1	
83	AL133292	3	140680	F13I12	471115	50364	50365	IND	1	-1/1	
83	AL133292	3	140680	F13I12	471116	63156	63158	IND	1	1/-1	
84	AL132955	3	101154	F1P2	466981	75142	75144	SNP	1		A/G
84	AL132955	3	101154	F1P2	467006	7386	7388	SNP	1		G/A
84	AL132955	3	101154	F1P2	467007	7160	7162	SNP	1		A/C
84	AL132955	3	101154	F1P2	467008	7323	7325	SNP	1		T/C
84	AL132955	3	101154	F1P2	467009	7483	7485	SNP	1		A/G
84	AL132955	3	101154	F1P2	467291	62676	62678	SNP	1		A/G
84	AL132955	3	101154	F1P2	467410	24858	24860	SNP	1		A/G
84	AL132955	3	101154	F1P2	468339	59827	59829	SNP	1		G/A
84	AL132955	3	101154	F1P2	468340	59552	59554	SNP	1		G/A
84	AL132955	3	101154	F1P2	468341	59729	59731	SNP	1		G/A
84	AL132955	3	101154	F1P2	468342	59743	59745	SNP	1		A/G
84	AL132955	3	101154	F1P2	468343	59846	59848	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
84	AL132955	3	101154	F1P2	468449	912	914	SNP	1		A/G
84	AL132955	3	101154	F1P2	468744	82100	82102	SNP	1		T/A
84	AL132955	3	101154	F1P2	468745	81920	81922	SNP	1		G/A
84	AL132955	3	101154	F1P2	468746	82513	82515	SNP	1		T/C
84	AL132955	3	101154	F1P2	468747	81967	81969	SNP	1		T/G
84	AL132955	3	101154	F1P2	468748	81929	81931	SNP	1		C/G
84	AL132955	3	101154	F1P2	468749	82115	82117	SNP	1		G/T
84	AL132955	3	101154	F1P2	468973	25980	25982	SNP	1		T/C
84	AL132955	3	101154	F1P2	468974	26186	26188	SNP	1		C/T
84	AL132955	3	101154	F1P2	469433	51666	51668	SNP	1		G/A
84	AL132955	3	101154	F1P2	469845	35560	35571	IND	2	10/-10	
84	AL132955	3	101154	F1P2	469846	36346	36347	IND	2	-39/39	
84	AL132955	3	101154	F1P2	469847	66111	66157	IND	2	45/-45	
84	AL132955	3	101154	F1P2	469848	70889	70894	IND	2	4/-4	
84	AL132955	3	101154	F1P2	469849	71907	71915	IND	2	7/-7	
84	AL132955	3	101154	F1P2	469850	72421	72425	IND	2	3/-3	
84	AL132955	3	101154	F1P2	469851	73701	73702	IND	2	-9/9	
84	AL132955	3	101154	F1P2	469852	81201	81202	IND	2	-3/3	
84	AL132955	3	101154	F1P2	469853	81482	81483	IND	2	-3/3	
84	AL132955	3	101154	F1P2	469854	82152	82153	IND	2	-3/3	
84	AL132955	3	101154	F1P2	469855	84017	84082	IND	2	64/-64	
84	AL132955	3	101154	F1P2	469856	84719	84720	IND	2	-5/5	
84	AL132955	3	101154	F1P2	469857	84754	84755	IND	2	-4/4	
84	AL132955	3	101154	F1P2	469858	87825	87826	IND	2	-10/10	
84	AL132955	3	101154	F1P2	469859	89198	93127	IND	2	3928/-3928	
84	AL132955	3	101154	F1P2	469860	93648	93649	IND	2	-15/15	
84	AL132955	3	101154	F1P2	469861	94963	94964	IND	2	-4/4	
84	AL132955	3	101154	F1P2	471199	25963	25965	IND	1	1/-1	
84	AL132955	3	101154	F1P2	471200	59569	59571	IND	1	1/-1	
84	AL132955	3	101154	F1P2	471201	59571	59573	IND	1	1/-1	
84	AL132955	3	101154	F1P2	471202	59708	59709	IND	1	-1/1	
84	AL132955	3	101154	F1P2	471203	7463	7464	IND	1	-1/1	
84	AL132955	3	101154	F1P2	471204	7464	7465	IND	1	-1/1	
84	AL132955	3	101154	F1P2	471205	82165	82166	IND	1	-3/3	
85	AL133315	3	96679	T8P19	467027	40334	40336	SNP	1		A/C
85	AL133315	3	96679	T8P19	467118	36947	36949	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
85	AL133315	3	96679	T8P19	467119	36190	36192	SNP	1		A/T
85	AL133315	3	96679	T8P19	467221	29081	29083	SNP	1		G/A
85	AL133315	3	96679	T8P19	467222	29064	29066	SNP	1		G/A
85	AL133315	3	96679	T8P19	467265	46757	46759	SNP	1		A/T
85	AL133315	3	96679	T8P19	467266	47732	47734	SNP	1		A/T
85	AL133315	3	96679	T8P19	467400	1105	1107	SNP	1		G/C
85	AL133315	3	96679	T8P19	467401	1199	1201	SNP	1		G/C
85	AL133315	3	96679	T8P19	467648	26769	26771	SNP	1		G/A
85	AL133315	3	96679	T8P19	467649	26874	26876	SNP	1		A/T
85	AL133315	3	96679	T8P19	467696	5481	5483	SNP	1		G/A
85	AL133315	3	96679	T8P19	468100	76614	76616	SNP	1		C/T
85	AL133315	3	96679	T8P19	468450	64659	64661	SNP	1		G/T
85	AL133315	3	96679	T8P19	468809	67751	67753	SNP	1		T/G
85	AL133315	3	96679	T8P19	468843	50477	50479	SNP	1		C/A
85	AL133315	3	96679	T8P19	468844	50223	50225	SNP	1		G/A
85	AL133315	3	96679	T8P19	468845	50392	50394	SNP	1		T/C
85	AL133315	3	96679	T8P19	468846	50428	50430	SNP	1		A/G
85	AL133315	3	96679	T8P19	468847	50355	50357	SNP	1		C/G
85	AL133315	3	96679	T8P19	468848	50489	50491	SNP	1		C/T
85	AL133315	3	96679	T8P19	468849	50424	50426	SNP	1		G/T
85	AL133315	3	96679	T8P19	468850	50420	50422	SNP	1		A/T
85	AL133315	3	96679	T8P19	469221	48413	48415	SNP	1		A/G
85	AL133315	3	96679	T8P19	471042	12516	12520	IND	2	3/-3	
85	AL133315	3	96679	T8P19	471043	30508	30509	IND	2	-7/7	
85	AL133315	3	96679	T8P19	471044	36552	36553	IND	2	-3/3	
85	AL133315	3	96679	T8P19	471045	496	497	IND	2	-14/14	
85	AL133315	3	96679	T8P19	471046	54336	55482	IND	2	1145/-1145	
85	AL133315	3	96679	T8P19	471047	6346	6386	IND	2	39/-39	
85	AL133315	3	96679	T8P19	471048	64844	64869	IND	2	24/-24	
85	AL133315	3	96679	T8P19	471049	72586	72587	IND	2	-8/8	
85	AL133315	3	96679	T8P19	471050	72778	74418	IND	2	1639/-1639	
85	AL133315	3	96679	T8P19	471051	73035	74678	IND	2	1642/-1642	
85	AL133315	3	96679	T8P19	471052	83589	83590	IND	2	-15/15	
85	AL133315	3	96679	T8P19	471053	83590	83591	IND	2	-15/15	
85	AL133315	3	96679	T8P19	471054	88118	88123	IND	2	4/-4	
85	AL133315	3	96679	T8P19	471055	90816	91589	IND	2	772/-772	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
85	AL133315	3	96679	T8P19	471622	1162	1163	IND	1	-1/1	
85	AL133315	3	96679	T8P19	471623	12259	12260	IND	1	-1/1	
85	AL133315	3	96679	T8P19	471624	29078	29079	IND	1	-1/1	
85	AL133315	3	96679	T8P19	471625	29081	29082	IND	1	-1/1	
86	AL132963	3	82912	T21J18	467175	25733	25735	SNP	1		A/G
86	AL132963	3	82912	T21J18	467235	1513	1515	SNP	1		G/C
86	AL132963	3	82912	T21J18	467236	1583	1585	SNP	1		T/G
86	AL132963	3	82912	T21J18	467237	1576	1578	SNP	1		A/G
86	AL132963	3	82912	T21J18	467238	1330	1332	SNP	1		T/G
86	AL132963	3	82912	T21J18	467239	1581	1583	SNP	1		C/T
86	AL132963	3	82912	T21J18	467240	1560	1562	SNP	1		G/T
86	AL132963	3	82912	T21J18	467241	1143	1145	SNP	1		C/T
86	AL132963	3	82912	T21J18	467406	24057	24059	SNP	1		C/A
86	AL132963	3	82912	T21J18	467407	24045	24047	SNP	1		C/A
86	AL132963	3	82912	T21J18	467451	40917	40919	SNP	1		G/A
86	AL132963	3	82912	T21J18	467452	41278	41280	SNP	1		T/C
86	AL132963	3	82912	T21J18	467453	41405	41407	SNP	1		A/C
86	AL132963	3	82912	T21J18	467454	41088	41090	SNP	1		C/T
86	AL132963	3	82912	T21J18	467455	41493	41495	SNP	1		A/T
86	AL132963	3	82912	T21J18	467456	40214	40216	SNP	1		C/T
86	AL132963	3	82912	T21J18	467457	42713	42715	SNP	1		T/A
86	AL132963	3	82912	T21J18	467458	43277	43279	SNP	1		T/A
86	AL132963	3	82912	T21J18	467459	41635	41637	SNP	1		G/A
86	AL132963	3	82912	T21J18	467460	41644	41646	SNP	1		G/A
86	AL132963	3	82912	T21J18	467461	41646	41648	SNP	1		T/A
86	AL132963	3	82912	T21J18	467462	42323	42325	SNP	1		T/C
86	AL132963	3	82912	T21J18	467463	43324	43326	SNP	1		T/C
86	AL132963	3	82912	T21J18	467464	41623	41625	SNP	1		T/C
86	AL132963	3	82912	T21J18	467465	41634	41636	SNP	1		G/C
86	AL132963	3	82912	T21J18	467466	41645	41647	SNP	1		G/C
86	AL132963	3	82912	T21J18	467467	42242	42244	SNP	1		T/G
86	AL132963	3	82912	T21J18	467468	42688	42690	SNP	1		A/G
86	AL132963	3	82912	T21J18	467469	43135	43137	SNP	1		T/G
86	AL132963	3	82912	T21J18	467470	41636	41638	SNP	1		A/G
86	AL132963	3	82912	T21J18	467471	41637	41639	SNP	1		C/G
86	AL132963	3	82912	T21J18	467472	41639	41641	SNP	1		A/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
86	AL132963	3	82912	T21J18	467473	41650	41652	SNP	1		A/G
86	AL132963	3	82912	T21J18	467474	43278	43280	SNP	1		C/T
86	AL132963	3	82912	T21J18	467475	41630	41632	SNP	1		C/T
86	AL132963	3	82912	T21J18	467476	41632	41634	SNP	1		A/T
86	AL132963	3	82912	T21J18	467594	19859	19861	SNP	1		A/G
86	AL132963	3	82912	T21J18	467607	80961	80963	SNP	1		C/A
86	AL132963	3	82912	T21J18	467608	79075	79077	SNP	1		T/C
86	AL132963	3	82912	T21J18	467609	78885	78887	SNP	1		A/C
86	AL132963	3	82912	T21J18	467610	79802	79804	SNP	1		A/G
86	AL132963	3	82912	T21J18	467611	79215	79217	SNP	1		T/G
86	AL132963	3	82912	T21J18	467612	79888	79890	SNP	1		C/T
86	AL132963	3	82912	T21J18	467679	6759	6761	SNP	1		G/A
86	AL132963	3	82912	T21J18	468254	78419	78421	SNP	1		T/A
86	AL132963	3	82912	T21J18	468255	78172	78174	SNP	1		T/C
86	AL132963	3	82912	T21J18	468256	78050	78052	SNP	1		C/G
86	AL132963	3	82912	T21J18	468795	51259	51261	SNP	1		G/C
86	AL132963	3	82912	T21J18	469005	53455	53457	SNP	1		T/C
86	AL132963	3	82912	T21J18	469025	4617	4619	SNP	1		C/T
86	AL132963	3	82912	T21J18	469224	67974	67976	SNP	1		A/G
86	AL132963	3	82912	T21J18	469340	21452	21454	SNP	1		C/T
86	AL132963	3	82912	T21J18	469436	22630	22632	SNP	1		C/T
86	AL132963	3	82912	T21J18	469452	45147	45149	SNP	1		T/A
86	AL132963	3	82912	T21J18	469453	48112	48114	SNP	1		T/A
86	AL132963	3	82912	T21J18	469454	47975	47977	SNP	1		G/A
86	AL132963	3	82912	T21J18	469455	46757	46759	SNP	1		C/G
86	AL132963	3	82912	T21J18	470746	1002	1007	IND	2	4/-4	
86	AL132963	3	82912	T21J18	470747	25099	25100	IND	2	-3/3	
86	AL132963	3	82912	T21J18	470748	26738	26739	IND	2	-15/15	
86	AL132963	3	82912	T21J18	470749	27279	27287	IND	2	7/-7	
86	AL132963	3	82912	T21J18	470750	27638	27639	IND	2	-74/74	
86	AL132963	3	82912	T21J18	470751	33016	33025	IND	2	8/-8	
86	AL132963	3	82912	T21J18	470752	33634	33928	IND	2	293/-293	
86	AL132963	3	82912	T21J18	470753	3700	4473	IND	2	772/-772	
86	AL132963	3	82912	T21J18	470754	38450	41674	IND	2	3223/-3223	
86	AL132963	3	82912	T21J18	470755	38959	38971	IND	2	11/-11	
86	AL132963	3	82912	T21J18	470756	44920	44921	IND	2	-3/3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
86	AL132963	3	82912	T21J18	470757	49743	49790	IND	2	46/-46	
86	AL132963	3	82912	T21J18	470758	56189	56190	IND	2	-3/3	
86	AL132963	3	82912	T21J18	470759	56299	57022	IND	2	722/-722	
86	AL132963	3	82912	T21J18	470760	57903	57909	IND	2	5/-5	
86	AL132963	3	82912	T21J18	470761	59408	59431	IND	2	22/-22	
86	AL132963	3	82912	T21J18	470762	63819	63824	IND	2	4/-4	
86	AL132963	3	82912	T21J18	470763	65096	65097	IND	2	-10/10	
86	AL132963	3	82912	T21J18	470764	65492	65493	IND	2	-4/4	
86	AL132963	3	82912	T21J18	470765	65504	65505	IND	2	-8/8	
86	AL132963	3	82912	T21J18	470766	75921	75928	IND	2	6/-6	
86	AL132963	3	82912	T21J18	471498	1553	1554	IND	1	-1/1	
86	AL132963	3	82912	T21J18	471499	1873	1874	IND	1	-1/1	
86	AL132963	3	82912	T21J18	471500	19897	19900	IND	1	2/-2	
86	AL132963	3	82912	T21J18	471501	19924	19925	IND	1	-1/1	
86	AL132963	3	82912	T21J18	471502	21671	21672	IND	1	-1/1	
86	AL132963	3	82912	T21J18	471503	24059	24060	IND	1	-2/2	
86	AL132963	3	82912	T21J18	471504	24111	24112	IND	1	-1/1	
86	AL132963	3	82912	T21J18	471505	41308	41310	IND	1	1/-1	
86	AL132963	3	82912	T21J18	471506	41627	41629	IND	1	1/-1	
86	AL132963	3	82912	T21J18	471507	51367	51369	IND	1	1/-1	
86	AL132963	3	82912	T21J18	471508	6392	6395	IND	1	2/-2	
86	AL132963	3	82912	T21J18	471509	6677	6678	IND	1	-1/1	
86	AL132963	3	82912	T21J18	471510	81738	81740	IND	1	1/-1	
87	AL132967	3	85109	T2J13	467000	27927	27929	SNP	1		T/A
87	AL132967	3	85109	T2J13	467001	28643	28645	SNP	1		A/C
87	AL132967	3	85109	T2J13	467062	7254	7256	SNP	1		G/A
87	AL132967	3	85109	T2J13	467063	7699	7701	SNP	1		G/A
87	AL132967	3	85109	T2J13	467064	7704	7706	SNP	1		G/A
87	AL132967	3	85109	T2J13	467065	8028	8030	SNP	1		A/G
87	AL132967	3	85109	T2J13	467066	8137	8139	SNP	1		A/G
87	AL132967	3	85109	T2J13	468371	56681	56683	SNP	1		A/T
87	AL132967	3	85109	T2J13	469222	32316	32318	SNP	1		A/T
87	AL132967	3	85109	T2J13	470917	1034	1118	IND	2	83/-83	
87	AL132967	3	85109	T2J13	470918	18107	18108	IND	2	-7/7	
87	AL132967	3	85109	T2J13	470919	18109	18110	IND	2	-7/7	
87	AL132967	3	85109	T2J13	470920	25666	25667	IND	2	-7/7	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
87	AL132967	3	85109	T2J13	470921	26019	26023	IND	2	3/-3	
87	AL132967	3	85109	T2J13	470922	46627	46628	IND	2	-17/17	
87	AL132967	3	85109	T2J13	470923	64104	64105	IND	2	-10/10	
87	AL132967	3	85109	T2J13	471565	27890	27891	IND	1	-1/1	
88	AL132956	3	129757	F2K15	466930	80963	80965	SNP	1		G/A
88	AL132956	3	129757	F2K15	466931	80881	80883	SNP	1		A/G
88	AL132956	3	129757	F2K15	466933	30883	30885	SNP	1		T/C
88	AL132956	3	129757	F2K15	467117	19860	19862	SNP	1		C/A
88	AL132956	3	129757	F2K15	467366	32445	32447	SNP	1		A/T
88	AL132956	3	129757	F2K15	467550	26057	26059	SNP	1		A/G
88	AL132956	3	129757	F2K15	467551	125484	125486	SNP	1		T/A
88	AL132956	3	129757	F2K15	467552	126398	126400	SNP	1		C/A
88	AL132956	3	129757	F2K15	467553	126201	126203	SNP	1		G/A
88	AL132956	3	129757	F2K15	467554	125964	125966	SNP	1		T/C
88	AL132956	3	129757	F2K15	467555	125616	125618	SNP	1		T/C
88	AL132956	3	129757	F2K15	467556	126347	126349	SNP	1		G/C
88	AL132956	3	129757	F2K15	467557	126244	126246	SNP	1		T/C
88	AL132956	3	129757	F2K15	467558	125607	125609	SNP	1		A/G
88	AL132956	3	129757	F2K15	467559	125574	125576	SNP	1		A/G
88	AL132956	3	129757	F2K15	467560	125511	125513	SNP	1		T/G
88	AL132956	3	129757	F2K15	467561	125573	125575	SNP	1		C/T
88	AL132956	3	129757	F2K15	467562	125551	125553	SNP	1		C/T
88	AL132956	3	129757	F2K15	467692	52591	52593	SNP	1		G/A
88	AL132956	3	129757	F2K15	467693	52633	52635	SNP	1		C/A
88	AL132956	3	129757	F2K15	467694	52642	52644	SNP	1		A/T
88	AL132956	3	129757	F2K15	467695	52729	52731	SNP	1		C/T
88	AL132956	3	129757	F2K15	467917	53602	53604	SNP	1		T/C
88	AL132956	3	129757	F2K15	467918	53588	53590	SNP	1		T/G
88	AL132956	3	129757	F2K15	467919	53763	53765	SNP	1		C/T
88	AL132956	3	129757	F2K15	468194	54385	54387	SNP	1		A/C
88	AL132956	3	129757	F2K15	468195	55381	55383	SNP	1		A/G
88	AL132956	3	129757	F2K15	468196	54782	54784	SNP	1		A/G
88	AL132956	3	129757	F2K15	468197	54541	54543	SNP	1		A/T
88	AL132956	3	129757	F2K15	468198	54652	54654	SNP	1		G/T
88	AL132956	3	129757	F2K15	468199	54829	54831	SNP	1		C/T
88	AL132956	3	129757	F2K15	468200	57184	57186	SNP	1		T/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
88	AL132956	3	129757	F2K15	468201	56800	56802	SNP	1		C/A
88	AL132956	3	129757	F2K15	468202	56767	56769	SNP	1		G/A
88	AL132956	3	129757	F2K15	468203	57851	57853	SNP	1		G/A
88	AL132956	3	129757	F2K15	468204	57850	57852	SNP	1		G/A
88	AL132956	3	129757	F2K15	468205	56449	56451	SNP	1		T/C
88	AL132956	3	129757	F2K15	468206	57526	57528	SNP	1		T/C
88	AL132956	3	129757	F2K15	468207	57355	57357	SNP	1		A/G
88	AL132956	3	129757	F2K15	468208	57349	57351	SNP	1		A/G
88	AL132956	3	129757	F2K15	468209	57727	57729	SNP	1		C/G
88	AL132956	3	129757	F2K15	468210	57489	57491	SNP	1		C/G
88	AL132956	3	129757	F2K15	468211	58036	58038	SNP	1		C/T
88	AL132956	3	129757	F2K15	468212	57533	57535	SNP	1		G/T
88	AL132956	3	129757	F2K15	468213	57378	57380	SNP	1		C/T
88	AL132956	3	129757	F2K15	468315	63622	63624	SNP	1		T/C
88	AL132956	3	129757	F2K15	468520	58812	58814	SNP	1		T/C
88	AL132956	3	129757	F2K15	470165	102723	102732	IND	2	8/-8	
88	AL132956	3	129757	F2K15	470166	103802	103803	IND	2	-8/8	
88	AL132956	3	129757	F2K15	470167	111866	111867	IND	2	-10/10	
88	AL132956	3	129757	F2K15	470168	111871	111872	IND	2	-10/10	
88	AL132956	3	129757	F2K15	470169	114547	114554	IND	2	6/-6	
88	AL132956	3	129757	F2K15	470170	123467	123468	IND	2	-8/8	
88	AL132956	3	129757	F2K15	470171	126580	126585	IND	2	4/-4	
88	AL132956	3	129757	F2K15	470172	20970	21054	IND	2	83/-83	
88	AL132956	3	129757	F2K15	470173	27464	27474	IND	2	9/-9	
88	AL132956	3	129757	F2K15	470174	27508	27509	IND	2	-3/3	
88	AL132956	3	129757	F2K15	470175	27510	27511	IND	2	-3/3	
88	AL132956	3	129757	F2K15	470176	28037	28038	IND	2	-7/7	
88	AL132956	3	129757	F2K15	470177	3978	3979	IND	2	-7/7	
88	AL132956	3	129757	F2K15	470178	3980	3981	IND	2	-7/7	
88	AL132956	3	129757	F2K15	470179	61182	61207	IND	2	24/-24	
88	AL132956	3	129757	F2K15	470180	70283	70371	IND	2	87/-87	
88	AL132956	3	129757	F2K15	470181	72111	72129	IND	2	17/-17	
88	AL132956	3	129757	F2K15	470182	85070	85071	IND	2	-6/6	
88	AL132956	3	129757	F2K15	470183	85753	85754	IND	2	-13/13	
88	AL132956	3	129757	F2K15	470184	99225	99229	IND	2	3/-3	
88	AL132956	3	129757	F2K15	471301	52126	52127	IND	1	-1/1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg -1/1	SNP Base Columbia/ Landsberg
88	AL132956	3	129757	F2K15	471302	80719	80720	IND	1		
89	AL132964	3	104204	T9C5	467146	51630	51632	SNP	1		C/A
89	AL132964	3	104204	T9C5	467147	50490	50492	SNP	1		G/A
89	AL132964	3	104204	T9C5	467148	50381	50383	SNP	1		T/A
89	AL132964	3	104204	T9C5	467149	52325	52327	SNP	1		T/A
89	AL132964	3	104204	T9C5	467150	52332	52334	SNP	1		A/C
89	AL132964	3	104204	T9C5	467151	51624	51626	SNP	1		T/G
89	AL132964	3	104204	T9C5	467152	52401	52403	SNP	1		A/G
89	AL132964	3	104204	T9C5	467153	52364	52366	SNP	1		T/G
89	AL132964	3	104204	T9C5	467154	52411	52413	SNP	1		A/T
89	AL132964	3	104204	T9C5	467525	58478	58480	SNP	1		T/C
89	AL132964	3	104204	T9C5	467526	57621	57623	SNP	1		A/G
89	AL132964	3	104204	T9C5	467527	56667	56669	SNP	1		G/T
89	AL132964	3	104204	T9C5	467701	69089	69091	SNP	1		C/T
89	AL132964	3	104204	T9C5	468145	44206	44208	SNP	1		C/A
89	AL132964	3	104204	T9C5	468146	43974	43976	SNP	1		G/T
89	AL132964	3	104204	T9C5	468521	45744	45746	SNP	1		G/A
89	AL132964	3	104204	T9C5	468522	45698	45700	SNP	1		A/C
89	AL132964	3	104204	T9C5	468523	45863	45865	SNP	1		A/G
89	AL132964	3	104204	T9C5	468787	55440	55442	SNP	1		T/A
89	AL132964	3	104204	T9C5	468788	55956	55958	SNP	1		T/A
89	AL132964	3	104204	T9C5	468789	53905	53907	SNP	1		T/G
89	AL132964	3	104204	T9C5	468859	93557	93559	SNP	1		T/C
89	AL132964	3	104204	T9C5	468860	93383	93385	SNP	1		A/G
89	AL132964	3	104204	T9C5	468861	93622	93624	SNP	1		A/T
89	AL132964	3	104204	T9C5	468868	22895	22897	SNP	1		T/C
89	AL132964	3	104204	T9C5	468981	100659	100661	SNP	1		T/A
89	AL132964	3	104204	T9C5	468982	100429	100431	SNP	1		A/C
89	AL132964	3	104204	T9C5	468983	100797	100799	SNP	1		T/C
89	AL132964	3	104204	T9C5	468984	100729	100731	SNP	1		C/G
89	AL132964	3	104204	T9C5	468985	100978	100980	SNP	1		C/T
89	AL132964	3	104204	T9C5	469016	14576	14578	SNP	1		T/A
89	AL132964	3	104204	T9C5	469017	15440	15442	SNP	1		A/G
89	AL132964	3	104204	T9C5	469290	81746	81748	SNP	1		A/G
89	AL132964	3	104204	T9C5	469310	38077	38079	SNP	1		T/C
89	AL132964	3	104204	T9C5	469345	36816	36818	SNP	1		G/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
89	AL132964	3	104204	T9C5	469428	47426	47428	SNP	1		G/A
89	AL132964	3	104204	T9C5	469429	47041	47043	SNP	1		T/C
89	AL132964	3	104204	T9C5	471056	12100	12101	IND	2	-7/7	
89	AL132964	3	104204	T9C5	471057	16211	16218	IND	2	6/-6	
89	AL132964	3	104204	T9C5	471058	1855	1856	IND	2	-22/22	
89	AL132964	3	104204	T9C5	471059	2485	2486	IND	2	-3/3	
89	AL132964	3	104204	T9C5	471060	33580	33581	IND	2	-5/5	
89	AL132964	3	104204	T9C5	471061	35680	35681	IND	2	-3/3	
89	AL132964	3	104204	T9C5	471062	45128	45129	IND	2	-4/4	
89	AL132964	3	104204	T9C5	471063	48190	48191	IND	2	-5/5	
89	AL132964	3	104204	T9C5	471064	48815	48816	IND	2	-17/17	
89	AL132964	3	104204	T9C5	471065	51371	51372	IND	2	-6/6	
89	AL132964	3	104204	T9C5	471066	62716	62721	IND	2	4/-4	
89	AL132964	3	104204	T9C5	471067	66304	66305	IND	2	-3/3	
89	AL132964	3	104204	T9C5	471068	68119	68120	IND	2	-21/21	
89	AL132964	3	104204	T9C5	471069	70840	70841	IND	2	-8/8	
89	AL132964	3	104204	T9C5	471070	7387	7388	IND	2	-3/3	
89	AL132964	3	104204	T9C5	471071	76027	76036	IND	2	8/-8	
89	AL132964	3	104204	T9C5	471072	76579	76580	IND	2	-3/3	
89	AL132964	3	104204	T9C5	471073	9930	9937	IND	2	6/-6	
89	AL132964	3	104204	T9C5	471626	101152	101154	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471627	14308	14311	IND	1	2/-2	
89	AL132964	3	104204	T9C5	471628	15162	15163	IND	1	-1/1	
89	AL132964	3	104204	T9C5	471629	15241	15242	IND	1	-2/2	
89	AL132964	3	104204	T9C5	471630	47620	47653	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471631	47651	47653	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471632	50389	50391	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471633	51375	51376	IND	1	-6/6	
89	AL132964	3	104204	T9C5	471634	51651	51653	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471635	52387	52389	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471636	69055	69057	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471637	80492	80494	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471638	93373	93375	IND	1	1/-1	
89	AL132964	3	104204	T9C5	471639	93392	93394	IND	1	1/-1	
90	AL132965	3	97711	T16K5	466810	64801	64803	SNP	1		G/A
90	AL132965	3	97711	T16K5	466811	64400	64402	SNP	1		G/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
90	AL132965	3	97711	T16K5	466812	64638	64640	SNP	1		A/G
90	AL132965	3	97711	T16K5	466813	63373	63375	SNP	1		A/C
90	AL132965	3	97711	T16K5	467542	76666	76668	SNP	1		T/G
90	AL132965	3	97711	T16K5	467543	76918	76920	SNP	1		G/T
90	AL132965	3	97711	T16K5	467544	75838	75840	SNP	1		C/T
90	AL132965	3	97711	T16K5	467816	55185	55187	SNP	1		G/A
90	AL132965	3	97711	T16K5	468158	41744	41746	SNP	1		G/A
90	AL132965	3	97711	T16K5	468524	89188	89190	SNP	1		T/A
90	AL132965	3	97711	T16K5	468525	89021	89023	SNP	1		A/C
90	AL132965	3	97711	T16K5	468526	89299	89301	SNP	1		C/T
90	AL132965	3	97711	T16K5	468929	77380	77382	SNP	1		T/C
90	AL132965	3	97711	T16K5	468959	12894	12896	SNP	1		A/C
90	AL132965	3	97711	T16K5	470613	50458	50463	IND	2	4/-4	
90	AL132965	3	97711	T16K5	470614	57948	57949	IND	2	-3/3	
90	AL132965	3	97711	T16K5	470615	64268	64274	IND	2	5/-5	
90	AL132965	3	97711	T16K5	470616	70595	70596	IND	2	-10/10	
90	AL132965	3	97711	T16K5	470617	79147	79148	IND	2	-4/4	
90	AL132965	3	97711	T16K5	470618	96230	96240	IND	2	9/-9	
90	AL132965	3	97711	T16K5	470619	96287	96288	IND	2	-3/3	
90	AL132965	3	97711	T16K5	471439	17461	17463	IND	1	1/-1	
90	AL132965	3	97711	T16K5	471440	30290	30292	IND	1	1/-1	
90	AL132965	3	97711	T16K5	471441	64271	64275	IND	1	3/-3	
90	AL132965	3	97711	T16K5	471442	64275	64278	IND	1	2/-2	
90	AL132965	3	97711	T16K5	471443	76521	76523	IND	1	1/-1	
90	AL132965	3	97711	T16K5	471444	76535	76537	IND	1	1/-1	
91	AL132978	3	108158	F3A4	467653	70275	70277	SNP	1		T/C
91	AL132978	3	108158	F3A4	467673	11605	11607	SNP	1		C/T
91	AL132978	3	108158	F3A4	467674	11682	11684	SNP	1		C/T
91	AL132978	3	108158	F3A4	467675	10351	10353	SNP	1		T/C
91	AL132978	3	108158	F3A4	467676	11020	11022	SNP	1		T/G
91	AL132978	3	108158	F3A4	467722	67514	67516	SNP	1		G/A
91	AL132978	3	108158	F3A4	468265	65398	65400	SNP	1		G/A
91	AL132978	3	108158	F3A4	468309	59631	59633	SNP	1		G/A
91	AL132978	3	108158	F3A4	468310	59471	59473	SNP	1		T/G
91	AL132978	3	108158	F3A4	468364	41317	41319	SNP	1		C/T
91	AL132978	3	108158	F3A4	468365	41241	41243	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
91	AL132978	3	108158	F3A4	468388	7801	7803	SNP	1		G/A
91	AL132978	3	108158	F3A4	468642	64192	64194	SNP	1		T/A
91	AL132978	3	108158	F3A4	469364	52390	52392	SNP	1		C/T
91	AL132978	3	108158	F3A4	470200	14678	14682	IND	2	3/-3	
91	AL132978	3	108158	F3A4	470201	14767	14768	IND	2	-8/8	
91	AL132978	3	108158	F3A4	470202	14768	14769	IND	2	-8/8	
91	AL132978	3	108158	F3A4	470203	15986	15995	IND	2	8/-8	
91	AL132978	3	108158	F3A4	470204	18015	18026	IND	2	10/-10	
91	AL132978	3	108158	F3A4	470205	18100	18113	IND	2	12/-12	
91	AL132978	3	108158	F3A4	470206	26572	26576	IND	2	3/-3	
91	AL132978	3	108158	F3A4	470207	26623	26624	IND	2	-8/8	
91	AL132978	3	108158	F3A4	470208	3798	3808	IND	2	9/-9	
91	AL132978	3	108158	F3A4	470209	3855	3856	IND	2	-3/3	
91	AL132978	3	108158	F3A4	470210	56662	56663	IND	2	-11/11	
91	AL132978	3	108158	F3A4	470211	65857	65858	IND	2	-3/3	
91	AL132978	3	108158	F3A4	470212	66805	66813	IND	2	7/-7	
91	AL132978	3	108158	F3A4	470213	8393	8394	IND	2	-6/6	
91	AL132978	3	108158	F3A4	470214	90509	90535	IND	2	25/-25	
91	AL132978	3	108158	F3A4	470215	92208	92209	IND	2	-3/3	
91	AL132978	3	108158	F3A4	471307	10792	10793	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471308	29729	29730	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471309	29806	29807	IND	1	-2/2	
91	AL132978	3	108158	F3A4	471310	41274	41275	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471311	6678	6679	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471312	67033	67034	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471313	7505	7506	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471314	7514	7515	IND	1	-1/1	
91	AL132978	3	108158	F3A4	471315	8394	8395	IND	1	-6/6	
92	AL132976	3	105644	F11C1	466904	65943	65945	SNP	1		A/G
92	AL132976	3	105644	F11C1	467535	51717	51719	SNP	1		A/T
92	AL132976	3	105644	F11C1	467615	95291	95293	SNP	1		T/A
92	AL132976	3	105644	F11C1	467644	35977	35979	SNP	1		T/C
92	AL132976	3	105644	F11C1	467822	75594	75596	SNP	1		G/A
92	AL132976	3	105644	F11C1	467823	74536	74538	SNP	1		G/T
92	AL132976	3	105644	F11C1	467824	76701	76703	SNP	1		C/T
92	AL132976	3	105644	F11C1	467825	76682	76684	SNP	1		A/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
92	AL132976	3	105644	F11C1	467826	71967	71969	SNP	1		G/A
92	AL132976	3	105644	F11C1	467827	73217	73219	SNP	1		T/A
92	AL132976	3	105644	F11C1	467828	73384	73386	SNP	1		A/C
92	AL132976	3	105644	F11C1	467829	72513	72515	SNP	1		A/G
92	AL132976	3	105644	F11C1	467934	34350	34352	SNP	1		A/G
92	AL132976	3	105644	F11C1	467971	91403	91405	SNP	1		T/C
92	AL132976	3	105644	F11C1	467972	91418	91420	SNP	1		A/G
92	AL132976	3	105644	F11C1	467973	91208	91210	SNP	1		A/T
92	AL132976	3	105644	F11C1	468078	82990	82992	SNP	1		G/A
92	AL132976	3	105644	F11C1	468118	80120	80122	SNP	1		A/G
92	AL132976	3	105644	F11C1	468536	103048	103050	SNP	1		T/A
92	AL132976	3	105644	F11C1	468537	103375	103377	SNP	1		T/C
92	AL132976	3	105644	F11C1	468538	102732	102734	SNP	1		T/C
92	AL132976	3	105644	F11C1	468539	102703	102705	SNP	1		C/T
92	AL132976	3	105644	F11C1	468540	102715	102717	SNP	1		G/T
92	AL132976	3	105644	F11C1	468541	102735	102737	SNP	1		C/T
92	AL132976	3	105644	F11C1	468542	102793	102795	SNP	1		A/T
92	AL132976	3	105644	F11C1	468543	103093	103095	SNP	1		C/T
92	AL132976	3	105644	F11C1	468796	43122	43124	SNP	1		A/T
92	AL132976	3	105644	F11C1	469231	38828	38830	SNP	1		T/G
92	AL132976	3	105644	F11C1	469232	45854	45856	SNP	1		C/T
92	AL132976	3	105644	F11C1	469233	40590	40592	SNP	1		T/C
92	AL132976	3	105644	F11C1	469235	94339	94341	SNP	1		T/A
92	AL132976	3	105644	F11C1	469236	94536	94538	SNP	1		G/T
92	AL132976	3	105644	F11C1	469411	99012	99014	SNP	1		T/C
92	AL132976	3	105644	F11C1	469494	101583	101584	IND	2	-6/6	
92	AL132976	3	105644	F11C1	469495	101916	101921	IND	2	4/-4	
92	AL132976	3	105644	F11C1	469496	104311	104312	IND	2	-24/24	
92	AL132976	3	105644	F11C1	469497	105093	105094	IND	2	-8/8	
92	AL132976	3	105644	F11C1	469498	2484	12962	IND	2	10477/-10477	
92	AL132976	3	105644	F11C1	469499	30519	30537	IND	2	17/-17	
92	AL132976	3	105644	F11C1	469500	30769	30787	IND	2	17/-17	
92	AL132976	3	105644	F11C1	469501	30772	30773	IND	2	-6/6	
92	AL132976	3	105644	F11C1	469502	47460	47465	IND	2	4/-4	
92	AL132976	3	105644	F11C1	469503	47577	47578	IND	2	-11/11	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
92	AL132976	3	105644	F11C1	469504	53711	53718	IND	2	6/-6	
92	AL132976	3	105644	F11C1	469505	53713	53718	IND	2	4/-4	
92	AL132976	3	105644	F11C1	469506	64837	64844	IND	2	6/-6	
92	AL132976	3	105644	F11C1	469507	64862	64869	IND	2	6/-6	
92	AL132976	3	105644	F11C1	469508	69147	69148	IND	2	-14/14	
92	AL132976	3	105644	F11C1	469509	97568	97569	IND	2	-5/5	
92	AL132976	3	105644	F11C1	471082	14670	14671	IND	1	-1/1	
92	AL132976	3	105644	F11C1	471083	34296	34297	IND	1	-1/1	
92	AL132976	3	105644	F11C1	471084	67140	67142	IND	1	1/-1	
92	AL132976	3	105644	F11C1	471085	71271	71272	IND	1	-1/1	
92	AL132976	3	105644	F11C1	471086	73369	73371	IND	1	1/-1	
92	AL132976	3	105644	F11C1	471087	73371	73373	IND	1	1/-1	
92	AL132976	3	105644	F11C1	471088	73906	73907	IND	1	-2/2	
92	AL132976	3	105644	F11C1	471089	94138	94139	IND	1	-2/2	
93	AL133363	3	83513	T20E23	467035	12171	12173	SNP	1		T/C
93	AL133363	3	83513	T20E23	467087	59551	59553	SNP	1		C/T
93	AL133363	3	83513	T20E23	467215	52932	52934	SNP	1		A/G
93	AL133363	3	83513	T20E23	467216	53015	53017	SNP	1		C/T
93	AL133363	3	83513	T20E23	467217	53246	53248	SNP	1		A/T
93	AL133363	3	83513	T20E23	468179	67768	67770	SNP	1		C/T
93	AL133363	3	83513	T20E23	468266	73518	73520	SNP	1		T/A
93	AL133363	3	83513	T20E23	468797	6700	6702	SNP	1		T/A
93	AL133363	3	83513	T20E23	468798	5522	5524	SNP	1		G/A
93	AL133363	3	83513	T20E23	468799	6399	6401	SNP	1		A/G
93	AL133363	3	83513	T20E23	468800	5843	5845	SNP	1		A/G
93	AL133363	3	83513	T20E23	468801	7200	7202	SNP	1		C/T
93	AL133363	3	83513	T20E23	468808	45932	45934	SNP	1		G/A
93	AL133363	3	83513	T20E23	468921	41573	41575	SNP	1		T/G
93	AL133363	3	83513	T20E23	469330	42699	42701	SNP	1		C/A
93	AL133363	3	83513	T20E23	469331	42741	42743	SNP	1		T/G
93	AL133363	3	83513	T20E23	469332	42853	42855	SNP	1		A/T
93	AL133363	3	83513	T20E23	469333	43305	43307	SNP	1		C/T
93	AL133363	3	83513	T20E23	470718	11222	11229	IND	2	6/-6	
93	AL133363	3	83513	T20E23	470719	11321	11326	IND	2	4/-4	
93	AL133363	3	83513	T20E23	470720	15043	15047	IND	2	3/-3	
93	AL133363	3	83513	T20E23	470721	27783	27798	IND	2	14/-14	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
93	AL133363	3	83513	T20E23	470722	27931	27935	IND	2	3/-3	
93	AL133363	3	83513	T20E23	470723	28582	28583	IND	2	-3/3	
93	AL133363	3	83513	T20E23	470724	64836	64837	IND	2	-24/24	
93	AL133363	3	83513	T20E23	470725	8687	8688	IND	2	-22/22	
93	AL133363	3	83513	T20E23	471484	42079	42082	IND	1	2/-2	
93	AL133363	3	83513	T20E23	471485	42987	42988	IND	1	-1/1	
93	AL133363	3	83513	T20E23	471486	43300	43301	IND	1	-1/1	
93	AL133363	3	83513	T20E23	471487	45147	45152	IND	1	4/-4	
93	AL133363	3	83513	T20E23	471488	53065	53066	IND	1	-1/1	
93	AL133363	3	83513	T20E23	471489	53248	53249	IND	1	-2/2	
93	AL133363	3	83513	T20E23	471490	5621	5622	IND	1	-1/1	
94	AL132979	3	84196	T3A5	467144	20014	20016	SNP	1		G/A
94	AL132979	3	84196	T3A5	467145	19733	19735	SNP	1		T/C
94	AL132979	3	84196	T3A5	467311	26955	26957	SNP	1		A/T
94	AL132979	3	84196	T3A5	467697	46422	46424	SNP	1		T/C
94	AL132979	3	84196	T3A5	467983	57880	57882	SNP	1		G/T
94	AL132979	3	84196	T3A5	468076	16665	16667	SNP	1		T/C
94	AL132979	3	84196	T3A5	468077	16801	16803	SNP	1		C/T
94	AL132979	3	84196	T3A5	468180	62356	62358	SNP	1		T/C
94	AL132979	3	84196	T3A5	468181	62496	62498	SNP	1		A/G
94	AL132979	3	84196	T3A5	468357	18188	18190	SNP	1		T/C
94	AL132979	3	84196	T3A5	468358	17892	17894	SNP	1		G/T
94	AL132979	3	84196	T3A5	468718	70356	70358	SNP	1		G/T
94	AL132979	3	84196	T3A5	468865	41140	41142	SNP	1		C/G
94	AL132979	3	84196	T3A5	469341	14914	14916	SNP	1		T/C
94	AL132979	3	84196	T3A5	470944	11653	11658	IND	2	4/-4	
94	AL132979	3	84196	T3A5	470945	11927	11944	IND	2	16/-16	
94	AL132979	3	84196	T3A5	470946	13529	13540	IND	2	10/-10	
94	AL132979	3	84196	T3A5	470947	42739	43756	IND	2	1016/-1016	
94	AL132979	3	84196	T3A5	470948	45968	45972	IND	2	3/-3	
94	AL132979	3	84196	T3A5	470949	51636	51642	IND	2	5/-5	
94	AL132979	3	84196	T3A5	470950	51994	51998	IND	2	3/-3	
94	AL132979	3	84196	T3A5	470951	5841	5848	IND	2	6/-6	
94	AL132979	3	84196	T3A5	470952	65523	65524	IND	2	-6/6	
94	AL132979	3	84196	T3A5	470953	76181	77186	IND	2	1004/-1004	
94	AL132979	3	84196	T3A5	470954	78009	78010	IND	2	-6/6	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
94	AL132979	3	84196	T3A5	470955	78014	78015	IND	2	-6/6	
94	AL132979	3	84196	T3A5	471574	14993	14994	IND	1	-1/1	
94	AL132979	3	84196	T3A5	471575	40954	40956	IND	1	1/-1	
94	AL132979	3	84196	T3A5	471576	45981	45985	IND	1	3/-3	
94	AL132979	3	84196	T3A5	471577	46618	46621	IND	1	2/-2	
94	AL132979	3	84196	T3A5	471578	62639	62640	IND	1	-1/1	
95	AL132980	3	129516	F24M12	466826	102169	102171	SNP	1		T/G
95	AL132980	3	129516	F24M12	466827	101968	101970	SNP	1		A/G
95	AL132980	3	129516	F24M12	466828	102142	102144	SNP	1		A/T
95	AL132980	3	129516	F24M12	467166	78437	78439	SNP	1		G/T
95	AL132980	3	129516	F24M12	467186	84795	84797	SNP	1		G/A
95	AL132980	3	129516	F24M12	467187	84810	84812	SNP	1		G/C
95	AL132980	3	129516	F24M12	467188	84804	84806	SNP	1		T/C
95	AL132980	3	129516	F24M12	467189	84793	84795	SNP	1		A/C
95	AL132980	3	129516	F24M12	467190	84789	84791	SNP	1		T/C
95	AL132980	3	129516	F24M12	467191	84813	84815	SNP	1		C/T
95	AL132980	3	129516	F24M12	467192	84507	84509	SNP	1		A/T
95	AL132980	3	129516	F24M12	467193	84439	84441	SNP	1		A/T
95	AL132980	3	129516	F24M12	467256	37398	37400	SNP	1		G/A
95	AL132980	3	129516	F24M12	467257	18924	18926	SNP	1		T/G
95	AL132980	3	129516	F24M12	467258	18809	18811	SNP	1		A/T
95	AL132980	3	129516	F24M12	467907	123951	123953	SNP	1		T/A
95	AL132980	3	129516	F24M12	467908	123728	123730	SNP	1		T/G
95	AL132980	3	129516	F24M12	468017	100640	100642	SNP	1		G/T
95	AL132980	3	129516	F24M12	468018	100630	100632	SNP	1		G/T
95	AL132980	3	129516	F24M12	468069	26307	26309	SNP	1		C/G
95	AL132980	3	129516	F24M12	468270	11401	11403	SNP	1		A/C
95	AL132980	3	129516	F24M12	468271	11831	11833	SNP	1		C/T
95	AL132980	3	129516	F24M12	468272	13034	13036	SNP	1		G/A
95	AL132980	3	129516	F24M12	468273	12993	12995	SNP	1		T/C
95	AL132980	3	129516	F24M12	468274	12782	12784	SNP	1		C/T
95	AL132980	3	129516	F24M12	468275	13473	13475	SNP	1		A/T
95	AL132980	3	129516	F24M12	468375	62111	62113	SNP	1		A/G
95	AL132980	3	129516	F24M12	468669	67143	67145	SNP	1		T/A
95	AL132980	3	129516	F24M12	468670	67360	67362	SNP	1		T/C
95	AL132980	3	129516	F24M12	468671	66898	66900	SNP	1		A/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
95	AL132980	3	129516	F24M12	468672	67136	67138	SNP	1		A/G
95	AL132980	3	129516	F24M12	468673	67080	67082	SNP	1		T/G
95	AL132980	3	129516	F24M12	468674	67561	67563	SNP	1		C/T
95	AL132980	3	129516	F24M12	468675	67075	67077	SNP	1		C/T
95	AL132980	3	129516	F24M12	468898	32317	32319	SNP	1		C/A
95	AL132980	3	129516	F24M12	468899	32267	32269	SNP	1		G/A
95	AL132980	3	129516	F24M12	468900	32138	32140	SNP	1		C/T
95	AL132980	3	129516	F24M12	468937	94559	94561	SNP	1		T/C
95	AL132980	3	129516	F24M12	468938	94140	94142	SNP	1		A/G
95	AL132980	3	129516	F24M12	469102	5857	5859	SNP	1		G/A
95	AL132980	3	129516	F24M12	469103	5860	5862	SNP	1		G/A
95	AL132980	3	129516	F24M12	469104	5931	5933	SNP	1		T/A
95	AL132980	3	129516	F24M12	469105	6419	6421	SNP	1		T/G
95	AL132980	3	129516	F24M12	469106	5930	5932	SNP	1		A/G
95	AL132980	3	129516	F24M12	469114	9642	9644	SNP	1		C/A
95	AL132980	3	129516	F24M12	469115	9585	9587	SNP	1		A/C
95	AL132980	3	129516	F24M12	469391	97879	97881	SNP	1		G/A
95	AL132980	3	129516	F24M12	469953	108797	108809	IND	2	11/-11	
95	AL132980	3	129516	F24M12	469954	111359	111360	IND	2	-24/24	
95	AL132980	3	129516	F24M12	469955	116736	116751	IND	2	14/-14	
95	AL132980	3	129516	F24M12	469956	116761	116776	IND	2	14/-14	
95	AL132980	3	129516	F24M12	469957	127477	127478	IND	2	-4/4	
95	AL132980	3	129516	F24M12	469958	128391	128402	IND	2	10/-10	
95	AL132980	3	129516	F24M12	469959	14334	14335	IND	2	-62/62	
95	AL132980	3	129516	F24M12	469960	40126	40140	IND	2	13/-13	
95	AL132980	3	129516	F24M12	469961	43488	43518	IND	2	29/-29	
95	AL132980	3	129516	F24M12	469962	52983	52984	IND	2	-10/10	
95	AL132980	3	129516	F24M12	469963	70556	70651	IND	2	94/-94	
95	AL132980	3	129516	F24M12	469964	72458	72467	IND	2	8/-8	
95	AL132980	3	129516	F24M12	469965	75636	75637	IND	2	-4/4	
95	AL132980	3	129516	F24M12	469966	76069	76070	IND	2	-72/72	
95	AL132980	3	129516	F24M12	469967	82861	82862	IND	2	-3/3	
95	AL132980	3	129516	F24M12	469968	98400	98401	IND	2	-5/5	
95	AL132980	3	129516	F24M12	471235	18727	18728	IND	1	-2/2	
95	AL132980	3	129516	F24M12	471236	37230	37232	IND	1	1/-1	
95	AL132980	3	129516	F24M12	471237	9180	9182	IND	1	1/-1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
95	AL132980	3	129516	F24M12	471238	9205	9206	IND	1	-2/2	
96	AL133452	3	94349	F26O13	467578	64269	64271	SNP	1		T/C
96	AL133452	3	94349	F26O13	467920	54007	54009	SNP	1		T/C
96	AL133452	3	94349	F26O13	468350	12615	12617	SNP	1		T/C
96	AL133452	3	94349	F26O13	468620	15987	15989	SNP	1		G/A
96	AL133452	3	94349	F26O13	470030	13873	13874	IND	2	-4/4	
96	AL133452	3	94349	F26O13	470031	14787	14798	IND	2	10/-10	
96	AL133452	3	94349	F26O13	470032	28418	28425	IND	2	6/-6	
96	AL133452	3	94349	F26O13	470033	30678	35715	IND	2	5036/-5036	
96	AL133452	3	94349	F26O13	470034	3132	3147	IND	2	14/-14	
96	AL133452	3	94349	F26O13	470035	3157	3172	IND	2	14/-14	
96	AL133452	3	94349	F26O13	470036	32198	32199	IND	2	-12/12	
96	AL133452	3	94349	F26O13	470037	33868	33869	IND	2	-8/8	
96	AL133452	3	94349	F26O13	470038	52385	52395	IND	2	9/-9	
96	AL133452	3	94349	F26O13	470039	52392	52402	IND	2	9/-9	
96	AL133452	3	94349	F26O13	470040	56628	56629	IND	2	-8/8	
96	AL133452	3	94349	F26O13	470041	66232	66239	IND	2	6/-6	
96	AL133452	3	94349	F26O13	470042	66672	66673	IND	2	-8/8	
96	AL133452	3	94349	F26O13	470043	77446	77465	IND	2	18/-18	
96	AL133452	3	94349	F26O13	470044	77467	77486	IND	2	18/-18	
96	AL133452	3	94349	F26O13	470045	83529	83534	IND	2	4/-4	
96	AL133452	3	94349	F26O13	470046	90694	90698	IND	2	3/-3	
97	AL132968	3	79867	T18N14	467242	65186	65188	SNP	1		C/A
97	AL132968	3	79867	T18N14	467243	65375	65377	SNP	1		T/A
97	AL132968	3	79867	T18N14	467244	65376	65378	SNP	1		T/A
97	AL132968	3	79867	T18N14	467245	66242	66244	SNP	1		A/G
97	AL132968	3	79867	T18N14	467246	66174	66176	SNP	1		G/T
97	AL132968	3	79867	T18N14	467598	17739	17741	SNP	1		G/C
97	AL132968	3	79867	T18N14	467664	49059	49061	SNP	1		T/A
97	AL132968	3	79867	T18N14	467665	49679	49681	SNP	1		C/A
97	AL132968	3	79867	T18N14	467666	49057	49059	SNP	1		G/C
97	AL132968	3	79867	T18N14	467667	49231	49233	SNP	1		T/C
97	AL132968	3	79867	T18N14	467668	49303	49305	SNP	1		A/G
97	AL132968	3	79867	T18N14	467761	61326	61328	SNP	1		A/G
97	AL132968	3	79867	T18N14	467762	61340	61342	SNP	1		A/G
97	AL132968	3	79867	T18N14	467763	57984	57986	SNP	1		G/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
97	AL132968	3	79867	T18N14	467764	57833	57835	SNP	1		G/A
97	AL132968	3	79867	T18N14	467765	57939	57941	SNP	1		T/C
97	AL132968	3	79867	T18N14	467766	57924	57926	SNP	1		C/G
97	AL132968	3	79867	T18N14	467767	58203	58205	SNP	1		G/T
97	AL132968	3	79867	T18N14	468220	19097	19099	SNP	1		G/A
97	AL132968	3	79867	T18N14	468221	20009	20011	SNP	1		A/C
97	AL132968	3	79867	T18N14	468222	19525	19527	SNP	1		T/C
97	AL132968	3	79867	T18N14	468223	19261	19263	SNP	1		T/G
97	AL132968	3	79867	T18N14	468224	20330	20332	SNP	1		A/T
97	AL132968	3	79867	T18N14	468225	19454	19456	SNP	1		G/T
97	AL132968	3	79867	T18N14	468326	63255	63257	SNP	1		A/G
97	AL132968	3	79867	T18N14	468327	63437	63439	SNP	1		G/T
97	AL132968	3	79867	T18N14	468436	30135	30137	SNP	1		C/A
97	AL132968	3	79867	T18N14	468437	30256	30258	SNP	1		T/A
97	AL132968	3	79867	T18N14	468438	30257	30259	SNP	1		G/A
97	AL132968	3	79867	T18N14	468439	29668	29670	SNP	1		G/T
97	AL132968	3	79867	T18N14	468440	30087	30089	SNP	1		C/T
97	AL132968	3	79867	T18N14	468666	24775	24777	SNP	1		C/A
97	AL132968	3	79867	T18N14	468780	4810	4812	SNP	1		T/A
97	AL132968	3	79867	T18N14	469080	28024	28026	SNP	1		G/A
97	AL132968	3	79867	T18N14	469081	27942	27944	SNP	1		A/T
97	AL132968	3	79867	T18N14	469334	56421	56423	SNP	1		T/A
97	AL132968	3	79867	T18N14	469335	56052	56054	SNP	1		C/T
97	AL132968	3	79867	T18N14	469468	71005	71007	SNP	1		A/G
97	AL132968	3	79867	T18N14	469469	70220	70222	SNP	1		C/T
97	AL132968	3	79867	T18N14	469470	71132	71134	SNP	1		C/T
97	AL132968	3	79867	T18N14	470659	12925	12944	IND	2	18/-18	
97	AL132968	3	79867	T18N14	470660	12946	12965	IND	2	18/-18	
97	AL132968	3	79867	T18N14	470661	1711	1718	IND	2	6/-6	
97	AL132968	3	79867	T18N14	470662	19008	19013	IND	2	4/-4	
97	AL132968	3	79867	T18N14	470663	2151	2152	IND	2	-8/8	
97	AL132968	3	79867	T18N14	470664	26173	26177	IND	2	3/-3	
97	AL132968	3	79867	T18N14	470665	30594	30595	IND	2	-10/10	
97	AL132968	3	79867	T18N14	470666	48282	48287	IND	2	4/-4	
97	AL132968	3	79867	T18N14	470667	53498	53499	IND	2	-3/3	
97	AL132968	3	79867	T18N14	470668	60781	60802	IND	2	20/-20	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
97	AL132968	3	79867	T18N14	470669	65667	65673	IND	2	5/-5	
97	AL132968	3	79867	T18N14	470670	79306	79319	IND	2	12/-12	
97	AL132968	3	79867	T18N14	470671	79310	79323	IND	2	12/-12	
97	AL132968	3	79867	T18N14	471460	19008	19011	IND	1	2/-2	
97	AL132968	3	79867	T18N14	471461	19011	19014	IND	1	2/-2	
97	AL132968	3	79867	T18N14	471462	24752	24753	IND	1	-1/1	
97	AL132968	3	79867	T18N14	471463	29619	29620	IND	1	-1/1	
97	AL132968	3	79867	T18N14	471464	29624	29625	IND	1	-3/3	
97	AL132968	3	79867	T18N14	471465	49149	49151	IND	1	1/-1	
97	AL132968	3	79867	T18N14	471466	49210	49212	IND	1	1/-1	
97	AL132968	3	79867	T18N14	471467	49224	49225	IND	1	-2/2	
97	AL132968	3	79867	T18N14	471468	63107	63108	IND	1	-1/1	
97	AL132968	3	79867	T18N14	471469	63172	63173	IND	1	-1/1	
97	AL132968	3	79867	T18N14	471470	65594	65597	IND	1	2/-2	
97	AL132968	3	79867	T18N14	471471	66172	66173	IND	1	-1/1	
98	AL132972	3	77350	T25B15	467815	32170	32172	SNP	1		A/G
98	AL132972	3	77350	T25B15	468164	53542	53544	SNP	1		T/A
98	AL132972	3	77350	T25B15	468165	55866	55868	SNP	1		T/C
98	AL132972	3	77350	T25B15	468166	56131	56133	SNP	1		C/G
98	AL132972	3	77350	T25B15	468167	56111	56113	SNP	1		G/T
98	AL132972	3	77350	T25B15	468374	28406	28408	SNP	1		G/T
98	AL132972	3	77350	T25B15	468555	18172	18174	SNP	1		A/C
98	AL132972	3	77350	T25B15	469018	65343	65345	SNP	1		T/A
98	AL132972	3	77350	T25B15	469019	65586	65588	SNP	1		A/T
98	AL132972	3	77350	T25B15	470856	42246	42265	IND	2	18/-18	
98	AL132972	3	77350	T25B15	471540	18231	18232	IND	1	-1/1	
98	AL132972	3	77350	T25B15	471541	65396	65397	IND	1	-1/1	
98	AL132972	3	77350	T25B15	471542	65453	65455	IND	1	1/-1	
99	AL132969	3	97798	F8J2	466797	12607	12609	SNP	1		T/A
99	AL132969	3	97798	F8J2	466798	13819	13821	SNP	1		A/G
99	AL132969	3	97798	F8J2	466799	13671	13673	SNP	1		G/T
99	AL132969	3	97798	F8J2	466829	17228	17230	SNP	1		C/T
99	AL132969	3	97798	F8J2	467141	67333	67335	SNP	1		T/C
99	AL132969	3	97798	F8J2	467142	66591	66593	SNP	1		C/G
99	AL132969	3	97798	F8J2	467159	207	209	SNP	1		G/A
99	AL132969	3	97798	F8J2	467160	486	488	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
99	AL132969	3	97798	F8J2	467161	478	480	SNP	1		A/C
99	AL132969	3	97798	F8J2	467162	163	165	SNP	1		A/G
99	AL132969	3	97798	F8J2	467163	482	484	SNP	1		A/T
99	AL132969	3	97798	F8J2	467164	476	478	SNP	1		A/T
99	AL132969	3	97798	F8J2	467165	157	159	SNP	1		A/T
99	AL132969	3	97798	F8J2	467196	2617	2619	SNP	1		G/A
99	AL132969	3	97798	F8J2	467197	2584	2586	SNP	1		T/A
99	AL132969	3	97798	F8J2	467230	65528	65530	SNP	1		C/T
99	AL132969	3	97798	F8J2	467373	7608	7610	SNP	1		T/C
99	AL132969	3	97798	F8J2	467374	7583	7585	SNP	1		A/T
99	AL132969	3	97798	F8J2	467502	47459	47461	SNP	1		C/A
99	AL132969	3	97798	F8J2	467503	47776	47778	SNP	1		T/C
99	AL132969	3	97798	F8J2	467504	47471	47473	SNP	1		C/T
99	AL132969	3	97798	F8J2	467563	78472	78474	SNP	1		C/G
99	AL132969	3	97798	F8J2	467700	90981	90983	SNP	1		C/A
99	AL132969	3	97798	F8J2	467958	69618	69620	SNP	1		T/G
99	AL132969	3	97798	F8J2	467970	42120	42122	SNP	1		A/G
99	AL132969	3	97798	F8J2	468131	50417	50419	SNP	1		T/A
99	AL132969	3	97798	F8J2	468132	50253	50255	SNP	1		A/T
99	AL132969	3	97798	F8J2	468313	24363	24365	SNP	1		A/T
99	AL132969	3	97798	F8J2	468323	56734	56736	SNP	1		C/A
99	AL132969	3	97798	F8J2	468329	34515	34517	SNP	1		A/T
99	AL132969	3	97798	F8J2	468514	19306	19308	SNP	1		T/C
99	AL132969	3	97798	F8J2	468604	16128	16130	SNP	1		G/A
99	AL132969	3	97798	F8J2	468605	16245	16247	SNP	1		C/G
99	AL132969	3	97798	F8J2	468727	89807	89809	SNP	1		C/G
99	AL132969	3	97798	F8J2	468728	89829	89831	SNP	1		G/T
99	AL132969	3	97798	F8J2	468729	89767	89769	SNP	1		C/T
99	AL132969	3	97798	F8J2	469026	73500	73502	SNP	1		T/G
99	AL132969	3	97798	F8J2	469054	5485	5487	SNP	1		C/G
99	AL132969	3	97798	F8J2	469055	5523	5525	SNP	1		A/T
99	AL132969	3	97798	F8J2	469056	5835	5837	SNP	1		A/T
99	AL132969	3	97798	F8J2	469057	5854	5856	SNP	1		A/T
99	AL132969	3	97798	F8J2	469116	55292	55294	SNP	1		C/T
99	AL132969	3	97798	F8J2	469159	94648	94650	SNP	1		A/C
99	AL132969	3	97798	F8J2	469160	94568	94570	SNP	1		A/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
99	AL132969	3	97798	F8J2	469161	94511	94513	SNP	1		A/G
99	AL132969	3	97798	F8J2	469162	94606	94608	SNP	1		G/T
99	AL132969	3	97798	F8J2	469163	94487	94489	SNP	1		C/T
99	AL132969	3	97798	F8J2	470385	10647	10694	IND	2	46/-46	
99	AL132969	3	97798	F8J2	470386	33793	33794	IND	2	-9/9	
99	AL132969	3	97798	F8J2	470387	35748	35749	IND	2	-3/3	
99	AL132969	3	97798	F8J2	470388	35823	35830	IND	2	6/-6	
99	AL132969	3	97798	F8J2	470389	52908	52915	IND	2	6/-6	
99	AL132969	3	97798	F8J2	470390	56618	56623	IND	2	4/-4	
99	AL132969	3	97798	F8J2	470391	77004	77014	IND	2	9/-9	
99	AL132969	3	97798	F8J2	470392	79524	79525	IND	2	-6/6	
99	AL132969	3	97798	F8J2	470393	81907	81908	IND	2	-14/14	
99	AL132969	3	97798	F8J2	471358	106	108	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471359	130	132	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471360	13308	13310	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471361	18051	18053	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471362	19472	19473	IND	1	-1/1	
99	AL132969	3	97798	F8J2	471363	23626	23628	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471364	24181	24183	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471365	24469	24470	IND	1	-1/1	
99	AL132969	3	97798	F8J2	471366	24692	24694	IND	1	1/-1	
99	AL132969	3	97798	F8J2	471367	50394	50395	IND	1	-1/1	
99	AL132969	3	97798	F8J2	471368	56621	56626	IND	1	4/-4	
99	AL132969	3	97798	F8J2	471369	67548	67549	IND	1	-1/1	
99	AL132969	3	97798	F8J2	471370	87728	87729	IND	1	-1/1	
99	AL132969	3	97798	F8J2	471371	89905	89906	IND	1	-1/1	
99	AL132969	3	97798	F8J2	471372	90861	90862	IND	1	-2/2	
99	AL132969	3	97798	F8J2	471373	94806	94809	IND	1	2/-2	
100	AL132958	3	92611	T4D2	466946	47899	47901	SNP	1		A/G
100	AL132958	3	92611	T4D2	466947	46953	46955	SNP	1		A/G
100	AL132958	3	92611	T4D2	467247	74748	74750	SNP	1		C/A
100	AL132958	3	92611	T4D2	467248	74822	74824	SNP	1		G/T
100	AL132958	3	92611	T4D2	467249	74823	74825	SNP	1		A/T
100	AL132958	3	92611	T4D2	467576	20878	20880	SNP	1		G/C
100	AL132958	3	92611	T4D2	467577	20977	20979	SNP	1		C/G
100	AL132958	3	92611	T4D2	467759	71118	71120	SNP	1		A/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
100	AL132958	3	92611	T4D2	467760	70203	70205	SNP	1		A/T
100	AL132958	3	92611	T4D2	467817	6227	6229	SNP	1		T/A
100	AL132958	3	92611	T4D2	467818	6332	6334	SNP	1		G/C
100	AL132958	3	92611	T4D2	467819	7957	7959	SNP	1		G/C
100	AL132958	3	92611	T4D2	467987	45056	45058	SNP	1		T/C
100	AL132958	3	92611	T4D2	467988	45051	45053	SNP	1		A/C
100	AL132958	3	92611	T4D2	467989	45036	45038	SNP	1		A/C
100	AL132958	3	92611	T4D2	467990	44625	44627	SNP	1		A/C
100	AL132958	3	92611	T4D2	467991	45037	45039	SNP	1		A/G
100	AL132958	3	92611	T4D2	467992	45024	45026	SNP	1		C/G
100	AL132958	3	92611	T4D2	467993	45039	45041	SNP	1		A/T
100	AL132958	3	92611	T4D2	467994	45017	45019	SNP	1		C/T
100	AL132958	3	92611	T4D2	467995	44616	44618	SNP	1		A/T
100	AL132958	3	92611	T4D2	468229	59566	59568	SNP	1		T/A
100	AL132958	3	92611	T4D2	468372	77474	77476	SNP	1		T/C
100	AL132958	3	92611	T4D2	468678	28382	28384	SNP	1		T/C
100	AL132958	3	92611	T4D2	468679	28200	28202	SNP	1		A/C
100	AL132958	3	92611	T4D2	468719	33653	33655	SNP	1		G/A
100	AL132958	3	92611	T4D2	468720	34570	34572	SNP	1		T/C
100	AL132958	3	92611	T4D2	468721	31906	31908	SNP	1		C/G
100	AL132958	3	92611	T4D2	468722	34097	34099	SNP	1		C/G
100	AL132958	3	92611	T4D2	468723	32544	32546	SNP	1		G/T
100	AL132958	3	92611	T4D2	468739	64243	64245	SNP	1		A/T
100	AL132958	3	92611	T4D2	468814	18494	18496	SNP	1		C/T
100	AL132958	3	92611	T4D2	469123	61962	61964	SNP	1		C/A
100	AL132958	3	92611	T4D2	469124	61881	61883	SNP	1		A/C
100	AL132958	3	92611	T4D2	469220	55485	55487	SNP	1		G/A
100	AL132958	3	92611	T4D2	470970	30621	30622	IND	2	-4/4	
100	AL132958	3	92611	T4D2	470971	30652	30653	IND	2	-10/10	
100	AL132958	3	92611	T4D2	470972	3264	3295	IND	2	30/-30	
100	AL132958	3	92611	T4D2	470973	40835	40847	IND	2	11/-11	
100	AL132958	3	92611	T4D2	470974	44201	44202	IND	2	-3/3	
100	AL132958	3	92611	T4D2	470975	51879	51889	IND	2	9/-9	
100	AL132958	3	92611	T4D2	470976	57125	57131	IND	2	5/-5	
100	AL132958	3	92611	T4D2	470977	70861	70869	IND	2	7/-7	
100	AL132958	3	92611	T4D2	470978	78960	78971	IND	2	10/-10	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
100	AL132958	3	92611	T4D2	470979	78988	78999	IND	2	10/-10	
100	AL132958	3	92611	T4D2	471581	14669	14671	IND	1	1/-1	
100	AL132958	3	92611	T4D2	471582	20164	20166	IND	1	1/-1	
100	AL132958	3	92611	T4D2	471583	28154	28156	IND	1	1/-1	
100	AL132958	3	92611	T4D2	471584	55615	55618	IND	1	2/-2	
101	AL132966	3	144628	F4P12	466952	68994	68996	SNP	1		G/A
101	AL132966	3	144628	F4P12	466953	73409	73411	SNP	1		A/C
101	AL132966	3	144628	F4P12	466954	72360	72362	SNP	1		A/G
101	AL132966	3	144628	F4P12	467098	46939	46941	SNP	1		G/T
101	AL132966	3	144628	F4P12	467178	99694	99696	SNP	1		T/G
101	AL132966	3	144628	F4P12	467179	104386	104388	SNP	1		A/G
101	AL132966	3	144628	F4P12	467180	105632	105634	SNP	1		A/T
101	AL132966	3	144628	F4P12	467299	59965	59967	SNP	1		C/A
101	AL132966	3	144628	F4P12	467300	60314	60316	SNP	1		A/G
101	AL132966	3	144628	F4P12	467301	41150	41152	SNP	1		G/A
101	AL132966	3	144628	F4P12	467436	88920	88922	SNP	1		G/A
101	AL132966	3	144628	F4P12	467497	66747	66749	SNP	1		A/C
101	AL132966	3	144628	F4P12	467662	55467	55469	SNP	1		G/A
101	AL132966	3	144628	F4P12	467663	55424	55426	SNP	1		A/C
101	AL132966	3	144628	F4P12	467732	110034	110036	SNP	1		C/A
101	AL132966	3	144628	F4P12	467733	110582	110584	SNP	1		G/A
101	AL132966	3	144628	F4P12	467734	109640	109642	SNP	1		G/T
101	AL132966	3	144628	F4P12	467801	80596	80598	SNP	1		A/T
101	AL132966	3	144628	F4P12	467874	94925	94927	SNP	1		T/C
101	AL132966	3	144628	F4P12	468169	65807	65809	SNP	1		A/T
101	AL132966	3	144628	F4P12	468253	26593	26595	SNP	1		A/T
101	AL132966	3	144628	F4P12	468461	10678	10680	SNP	1		T/G
101	AL132966	3	144628	F4P12	468480	137902	137904	SNP	1		G/A
101	AL132966	3	144628	F4P12	468481	137905	137907	SNP	1		T/A
101	AL132966	3	144628	F4P12	468482	137901	137903	SNP	1		G/C
101	AL132966	3	144628	F4P12	468975	28326	28328	SNP	1		C/T
101	AL132966	3	144628	F4P12	469168	82943	82945	SNP	1		G/A
101	AL132966	3	144628	F4P12	469175	51940	51942	SNP	1		C/A
101	AL132966	3	144628	F4P12	469176	51898	51900	SNP	1		C/T
101	AL132966	3	144628	F4P12	470278	109653	109657	IND	2	3/-3	
101	AL132966	3	144628	F4P12	470279	119554	119558	IND	2	3/-3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
101	AL132966	3	144628	F4P12	470280	129946	129956	IND	2	9/-9	
101	AL132966	3	144628	F4P12	470281	138877	138890	IND	2	12/-12	
101	AL132966	3	144628	F4P12	470282	139202	139203	IND	2	-7/7	
101	AL132966	3	144628	F4P12	470283	17351	20334	IND	2	2982/-2982	
101	AL132966	3	144628	F4P12	470284	18774	18795	IND	2	20/-20	
101	AL132966	3	144628	F4P12	470285	18780	18801	IND	2	20/-20	
101	AL132966	3	144628	F4P12	470286	19804	19833	IND	2	28/-28	
101	AL132966	3	144628	F4P12	470287	19806	19835	IND	2	28/-28	
101	AL132966	3	144628	F4P12	470288	28126	28132	IND	2	5/-5	
101	AL132966	3	144628	F4P12	470289	29112	29113	IND	2	-4/4	
101	AL132966	3	144628	F4P12	470290	31997	31998	IND	2	-3/3	
101	AL132966	3	144628	F4P12	470291	32003	32004	IND	2	-3/3	
101	AL132966	3	144628	F4P12	470292	33309	33319	IND	2	9/-9	
101	AL132966	3	144628	F4P12	470293	38758	38767	IND	2	8/-8	
101	AL132966	3	144628	F4P12	470294	45709	45710	IND	2	-5/5	
101	AL132966	3	144628	F4P12	470295	46419	46420	IND	2	-3/3	
101	AL132966	3	144628	F4P12	470296	48146	48152	IND	2	5/-5	
101	AL132966	3	144628	F4P12	470297	49192	49197	IND	2	4/-4	
101	AL132966	3	144628	F4P12	470298	57398	57399	IND	2	-3/3	
101	AL132966	3	144628	F4P12	470299	73019	73026	IND	2	6/-6	
101	AL132966	3	144628	F4P12	470300	77218	77219	IND	2	-24/24	
101	AL132966	3	144628	F4P12	470301	77238	77239	IND	2	-24/24	
101	AL132966	3	144628	F4P12	470302	81419	81423	IND	2	3/-3	
101	AL132966	3	144628	F4P12	471333	109658	109662	IND	1	3/-3	
101	AL132966	3	144628	F4P12	471334	22360	22361	IND	1	-1/1	
101	AL132966	3	144628	F4P12	471335	28129	28131	IND	1	1/-1	
101	AL132966	3	144628	F4P12	471336	28135	28140	IND	1	4/-4	
101	AL132966	3	144628	F4P12	471337	65803	65806	IND	1	2/-2	
101	AL132966	3	144628	F4P12	471338	66708	66709	IND	1	-1/1	
101	AL132966	3	144628	F4P12	471339	72814	72815	IND	1	-1/1	
101	AL132966	3	144628	F4P12	471340	73024	73027	IND	1	2/-2	
101	AL132966	3	144628	F4P12	471341	73029	73032	IND	1	2/-2	
101	AL132966	3	144628	F4P12	471342	95068	95069	IND	1	-1/1	
102	AL132960	3	112929	F5K20	467177	106867	106869	SNP	1		T/C
102	AL132960	3	112929	F5K20	467203	2244	2246	SNP	1		A/T
102	AL132960	3	112929	F5K20	467509	57787	57789	SNP	1		G/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
102	AL132960	3	112929	F5K20	467510	57855	57857	SNP	1		A/G
102	AL132960	3	112929	F5K20	467529	111605	111607	SNP	1		G/A
102	AL132960	3	112929	F5K20	467530	111500	111502	SNP	1		A/T
102	AL132960	3	112929	F5K20	467545	35458	35460	SNP	1		T/C
102	AL132960	3	112929	F5K20	467566	30815	30817	SNP	1		T/G
102	AL132960	3	112929	F5K20	467567	30932	30934	SNP	1		G/T
102	AL132960	3	112929	F5K20	467568	30934	30936	SNP	1		G/T
102	AL132960	3	112929	F5K20	467742	9596	9598	SNP	1		T/A
102	AL132960	3	112929	F5K20	467830	85621	85623	SNP	1		T/A
102	AL132960	3	112929	F5K20	467831	85122	85124	SNP	1		C/G
102	AL132960	3	112929	F5K20	467832	85061	85063	SNP	1		A/T
102	AL132960	3	112929	F5K20	467866	100414	100416	SNP	1		G/A
102	AL132960	3	112929	F5K20	468004	8706	8708	SNP	1		T/A
102	AL132960	3	112929	F5K20	468005	8055	8057	SNP	1		T/C
102	AL132960	3	112929	F5K20	468006	8752	8754	SNP	1		A/G
102	AL132960	3	112929	F5K20	468074	105428	105430	SNP	1		C/A
102	AL132960	3	112929	F5K20	469157	10428	10430	SNP	1		T/C
102	AL132960	3	112929	F5K20	469158	10540	10542	SNP	1		A/G
102	AL132960	3	112929	F5K20	469317	25821	25823	SNP	1		G/A
102	AL132960	3	112929	F5K20	469318	25087	25089	SNP	1		T/C
102	AL132960	3	112929	F5K20	469319	20121	20123	SNP	1		T/C
102	AL132960	3	112929	F5K20	469320	22901	22903	SNP	1		T/G
102	AL132960	3	112929	F5K20	469389	90023	90025	SNP	1		T/C
102	AL132960	3	112929	F5K20	469390	90211	90213	SNP	1		C/T
102	AL132960	3	112929	F5K20	469439	43417	43419	SNP	1		A/G
102	AL132960	3	112929	F5K20	469440	44004	44006	SNP	1		G/T
102	AL132960	3	112929	F5K20	470334	101849	101850	IND	2	-15/15	
102	AL132960	3	112929	F5K20	470335	1041	1042	IND	2	-7/7	
102	AL132960	3	112929	F5K20	470336	107410	107414	IND	2	3/-3	
102	AL132960	3	112929	F5K20	470337	108512	108513	IND	2	-6/6	
102	AL132960	3	112929	F5K20	470338	109025	109026	IND	2	-11/11	
102	AL132960	3	112929	F5K20	470339	29729	29740	IND	2	10/-10	
102	AL132960	3	112929	F5K20	470340	47233	47234	IND	2	-34/34	
102	AL132960	3	112929	F5K20	470341	54159	54173	IND	2	13/-13	
102	AL132960	3	112929	F5K20	470342	61920	61921	IND	2	-15/15	
102	AL132960	3	112929	F5K20	470343	61925	61926	IND	2	-15/15	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
102	AL132960	3	112929	F5K20	470344	68408	68409	IND	2	-3/3	
102	AL132960	3	112929	F5K20	470345	68409	68410	IND	2	-3/3	
102	AL132960	3	112929	F5K20	470346	716	729	IND	2	12/-12	
102	AL132960	3	112929	F5K20	470347	86085	86093	IND	2	7/-7	
102	AL132960	3	112929	F5K20	470348	96764	96768	IND	2	3/-3	
102	AL132960	3	112929	F5K20	471345	10429	10430	IND	1	-1/1	
102	AL132960	3	112929	F5K20	471346	25597	25599	IND	1	1/-1	
102	AL132960	3	112929	F5K20	471347	26006	26007	IND	1	-1/1	
102	AL132960	3	112929	F5K20	471348	30829	30831	IND	1	1/-1	
102	AL132960	3	112929	F5K20	471349	42927	42929	IND	1	1/-1	
102	AL132960	3	112929	F5K20	471350	56572	56574	IND	1	1/-1	
103	AL132957	3	100285	F24B22	466961	53823	53825	SNP	1		G/T
103	AL132957	3	100285	F24B22	466962	28612	28614	SNP	1		T/G
103	AL132957	3	100285	F24B22	467003	22290	22292	SNP	1		G/A
103	AL132957	3	100285	F24B22	467004	22167	22169	SNP	1		A/G
103	AL132957	3	100285	F24B22	467043	85754	85756	SNP	1		T/C
103	AL132957	3	100285	F24B22	467044	85653	85655	SNP	1		A/G
103	AL132957	3	100285	F24B22	467045	85056	85058	SNP	1		C/T
103	AL132957	3	100285	F24B22	467049	96223	96225	SNP	1		T/G
103	AL132957	3	100285	F24B22	467122	83731	83733	SNP	1		G/A
103	AL132957	3	100285	F24B22	467123	83927	83929	SNP	1		A/G
103	AL132957	3	100285	F24B22	467296	73058	73060	SNP	1		C/A
103	AL132957	3	100285	F24B22	467297	73181	73183	SNP	1		T/A
103	AL132957	3	100285	F24B22	467330	7480	7482	SNP	1		T/A
103	AL132957	3	100285	F24B22	467331	7649	7651	SNP	1		C/G
103	AL132957	3	100285	F24B22	467332	7629	7631	SNP	1		A/G
103	AL132957	3	100285	F24B22	467333	7614	7616	SNP	1		T/G
103	AL132957	3	100285	F24B22	467334	7606	7608	SNP	1		T/G
103	AL132957	3	100285	F24B22	467335	7616	7618	SNP	1		A/T
103	AL132957	3	100285	F24B22	467515	46543	46545	SNP	1		C/T
103	AL132957	3	100285	F24B22	467620	30613	30615	SNP	1		T/G
103	AL132957	3	100285	F24B22	468087	59338	59340	SNP	1		T/C
103	AL132957	3	100285	F24B22	468088	60141	60143	SNP	1		A/G
103	AL132957	3	100285	F24B22	468466	82701	82703	SNP	1		G/A
103	AL132957	3	100285	F24B22	468467	82824	82826	SNP	1		T/C
103	AL132957	3	100285	F24B22	468468	81717	81719	SNP	1		T/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
103	AL132957	3	100285	F24B22	468469	83050	83052	SNP	1		A/G
103	AL132957	3	100285	F24B22	468470	82607	82609	SNP	1		G/T
103	AL132957	3	100285	F24B22	468904	19846	19848	SNP	1		C/A
103	AL132957	3	100285	F24B22	468905	19284	19286	SNP	1		A/C
103	AL132957	3	100285	F24B22	468906	19706	19708	SNP	1		C/G
103	AL132957	3	100285	F24B22	468922	3930	3932	SNP	1		G/A
103	AL132957	3	100285	F24B22	468923	3856	3858	SNP	1		A/G
103	AL132957	3	100285	F24B22	468924	3796	3798	SNP	1		A/G
103	AL132957	3	100285	F24B22	468925	3648	3650	SNP	1		C/G
103	AL132957	3	100285	F24B22	468926	4888	4890	SNP	1		C/T
103	AL132957	3	100285	F24B22	468927	4419	4421	SNP	1		G/T
103	AL132957	3	100285	F24B22	468928	4074	4076	SNP	1		C/T
103	AL132957	3	100285	F24B22	468955	58258	58260	SNP	1		A/G
103	AL132957	3	100285	F24B22	468956	58351	58353	SNP	1		C/T
103	AL132957	3	100285	F24B22	468957	56388	56390	SNP	1		T/C
103	AL132957	3	100285	F24B22	468958	57372	57374	SNP	1		A/G
103	AL132957	3	100285	F24B22	468969	16897	16899	SNP	1		T/C
103	AL132957	3	100285	F24B22	469035	93312	93314	SNP	1		G/A
103	AL132957	3	100285	F24B22	469036	93621	93623	SNP	1		C/T
103	AL132957	3	100285	F24B22	469088	64198	64200	SNP	1		T/C
103	AL132957	3	100285	F24B22	469305	70800	70802	SNP	1		T/A
103	AL132957	3	100285	F24B22	469306	70794	70796	SNP	1		A/G
103	AL132957	3	100285	F24B22	469346	86682	86684	SNP	1		T/A
103	AL132957	3	100285	F24B22	469347	86516	86518	SNP	1		G/T
103	AL132957	3	100285	F24B22	469456	71834	71836	SNP	1		C/T
103	AL132957	3	100285	F24B22	469888	1071	1072	IND	2	-3/3	
103	AL132957	3	100285	F24B22	469889	34715	34720	IND	2	4/-4	
103	AL132957	3	100285	F24B22	469890	502	509	IND	2	6/-6	
103	AL132957	3	100285	F24B22	469891	65587	65594	IND	2	6/-6	
103	AL132957	3	100285	F24B22	469892	78100	78202	IND	2	101/-101	
103	AL132957	3	100285	F24B22	469893	78888	78895	IND	2	6/-6	
103	AL132957	3	100285	F24B22	469894	89415	89427	IND	2	11/-11	
103	AL132957	3	100285	F24B22	469895	89480	89481	IND	2	-7/7	
103	AL132957	3	100285	F24B22	469896	90002	90003	IND	2	-9/9	
103	AL132957	3	100285	F24B22	469897	90005	90006	IND	2	-9/9	
103	AL132957	3	100285	F24B22	469898	90997	90998	IND	2	-13/13	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
103	AL132957	3	100285	F24B22	469899	91401	91402	IND	2	-7/7	
103	AL132957	3	100285	F24B22	469900	91504	91514	IND	2	9/-9	
103	AL132957	3	100285	F24B22	469901	9396	9397	IND	2	-5/5	
103	AL132957	3	100285	F24B22	471214	16900	16901	IND	1	-1/1	
103	AL132957	3	100285	F24B22	471215	22287	22288	IND	1	-1/1	
103	AL132957	3	100285	F24B22	471216	30310	30311	IND	1	-1/1	
103	AL132957	3	100285	F24B22	471217	34715	34717	IND	1	1/-1	
103	AL132957	3	100285	F24B22	471218	34717	34721	IND	1	3/-3	
103	AL132957	3	100285	F24B22	471219	44889	44892	IND	1	2/-2	
103	AL132957	3	100285	F24B22	471220	63622	63624	IND	1	1/-1	
103	AL132957	3	100285	F24B22	471221	71930	71932	IND	1	1/-1	
103	AL132957	3	100285	F24B22	471222	7669	7672	IND	1	2/-2	
104	AL132971	3	40766	T12E18	470576	5268	5273	IND	2	4/-4	
104	AL132971	3	40766	T12E18	470577	6621	6622	IND	2	-3/3	
105	AL132970	3	84233	T15C9	466837	65726	65728	SNP	1		G/A
105	AL132970	3	84233	T15C9	466838	64553	64555	SNP	1		A/C
105	AL132970	3	84233	T15C9	466880	13411	13413	SNP	1		A/G
105	AL132970	3	84233	T15C9	466881	13409	13411	SNP	1		C/T
105	AL132970	3	84233	T15C9	466899	51283	51285	SNP	1		C/A
105	AL132970	3	84233	T15C9	467231	58240	58242	SNP	1		T/C
105	AL132970	3	84233	T15C9	467810	594	596	SNP	1		T/A
105	AL132970	3	84233	T15C9	467811	1028	1030	SNP	1		G/T
105	AL132970	3	84233	T15C9	467869	8694	8696	SNP	1		G/A
105	AL132970	3	84233	T15C9	467870	8806	8808	SNP	1		A/G
105	AL132970	3	84233	T15C9	467974	74558	74560	SNP	1		G/T
105	AL132970	3	84233	T15C9	468127	52919	52921	SNP	1		G/A
105	AL132970	3	84233	T15C9	468128	52245	52247	SNP	1		C/A
105	AL132970	3	84233	T15C9	468556	75060	75062	SNP	1		G/T
105	AL132970	3	84233	T15C9	468577	11851	11853	SNP	1		A/C
105	AL132970	3	84233	T15C9	469090	83502	83504	SNP	1		G/A
105	AL132970	3	84233	T15C9	469091	83055	83057	SNP	1		A/C
105	AL132970	3	84233	T15C9	469092	83145	83147	SNP	1		C/G
105	AL132970	3	84233	T15C9	469093	82828	82830	SNP	1		T/G
105	AL132970	3	84233	T15C9	469094	82877	82879	SNP	1		T/G
105	AL132970	3	84233	T15C9	469095	82943	82945	SNP	1		A/T
105	AL132970	3	84233	T15C9	469096	82239	82241	SNP	1		A/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
105	AL132970	3	84233	T15C9	469097	82617	82619	SNP	1		G/T
105	AL132970	3	84233	T15C9	469098	82655	82657	SNP	1		C/T
105	AL132970	3	84233	T15C9	469099	82876	82878	SNP	1		G/T
105	AL132970	3	84233	T15C9	470600	20698	20703	IND	2	4/-4	
105	AL132970	3	84233	T15C9	470601	23054	23055	IND	2	-4/4	
105	AL132970	3	84233	T15C9	470602	38775	38785	IND	2	9/-9	
105	AL132970	3	84233	T15C9	470603	39764	39774	IND	2	9/-9	
105	AL132970	3	84233	T15C9	470604	40002	40007	IND	2	4/-4	
105	AL132970	3	84233	T15C9	470605	42745	42746	IND	2	-3/3	
105	AL132970	3	84233	T15C9	470606	42888	42889	IND	2	-3/3	
105	AL132970	3	84233	T15C9	470607	47779	47798	IND	2	18/-18	
105	AL132970	3	84233	T15C9	470608	5443	5444	IND	2	-3/3	
105	AL132970	3	84233	T15C9	470609	68804	68816	IND	2	11/-11	
105	AL132970	3	84233	T15C9	470610	68805	68817	IND	2	11/-11	
105	AL132970	3	84233	T15C9	470611	73029	73030	IND	2	-28/28	
105	AL132970	3	84233	T15C9	470612	81439	81444	IND	2	4/-4	
105	AL132970	3	84233	T15C9	471438	50544	50545	IND	1	-1/1	
106	AL132954	3	88997	T26I12	466878	72880	72882	SNP	1		A/T
106	AL132954	3	88997	T26I12	466894	15266	15268	SNP	1		T/C
106	AL132954	3	88997	T26I12	466895	15744	15746	SNP	1		A/G
106	AL132954	3	88997	T26I12	466900	14670	14672	SNP	1		T/A
106	AL132954	3	88997	T26I12	466901	14649	14651	SNP	1		C/G
106	AL132954	3	88997	T26I12	467404	42566	42568	SNP	1		C/G
106	AL132954	3	88997	T26I12	467405	42409	42411	SNP	1		A/T
106	AL132954	3	88997	T26I12	467445	19759	19761	SNP	1		G/A
106	AL132954	3	88997	T26I12	467446	19246	19248	SNP	1		T/A
106	AL132954	3	88997	T26I12	467447	19658	19660	SNP	1		A/G
106	AL132954	3	88997	T26I12	467448	19534	19536	SNP	1		A/G
106	AL132954	3	88997	T26I12	467449	19807	19809	SNP	1		A/T
106	AL132954	3	88997	T26I12	467450	19776	19778	SNP	1		A/T
106	AL132954	3	88997	T26I12	467698	9390	9392	SNP	1		T/C
106	AL132954	3	88997	T26I12	467729	87405	87407	SNP	1		T/A
106	AL132954	3	88997	T26I12	468136	69434	69436	SNP	1		G/A
106	AL132954	3	88997	T26I12	468519	88285	88287	SNP	1		T/G
106	AL132954	3	88997	T26I12	468557	4025	4027	SNP	1		G/A
106	AL132954	3	88997	T26I12	468558	4447	4449	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
106	AL132954	3	88997	T26I12	468559	4247	4249	SNP	1		T/C
106	AL132954	3	88997	T26I12	468560	4783	4785	SNP	1		C/G
106	AL132954	3	88997	T26I12	468561	4446	4448	SNP	1		T/G
106	AL132954	3	88997	T26I12	468562	4223	4225	SNP	1		C/T
106	AL132954	3	88997	T26I12	468939	10026	10028	SNP	1		G/A
106	AL132954	3	88997	T26I12	468940	10113	10115	SNP	1		C/T
106	AL132954	3	88997	T26I12	468979	7365	7367	SNP	1		T/C
106	AL132954	3	88997	T26I12	468980	7273	7275	SNP	1		T/C
106	AL132954	3	88997	T26I12	469010	14012	14014	SNP	1		C/A
106	AL132954	3	88997	T26I12	469011	13745	13747	SNP	1		T/A
106	AL132954	3	88997	T26I12	469012	13846	13848	SNP	1		T/C
106	AL132954	3	88997	T26I12	469013	14156	14158	SNP	1		G/C
106	AL132954	3	88997	T26I12	470874	11413	11420	IND	2	6/-6	
106	AL132954	3	88997	T26I12	470875	22607	22608	IND	2	-6/6	
106	AL132954	3	88997	T26I12	470876	23943	23944	IND	2	-11/11	
106	AL132954	3	88997	T26I12	470877	33857	33858	IND	2	-14/14	
106	AL132954	3	88997	T26I12	470878	34940	35329	IND	2	388/-388	
106	AL132954	3	88997	T26I12	470879	40014	40031	IND	2	16/-16	
106	AL132954	3	88997	T26I12	470880	43066	43067	IND	2	-3/3	
106	AL132954	3	88997	T26I12	470881	44196	44213	IND	2	16/-16	
106	AL132954	3	88997	T26I12	470882	46955	46962	IND	2	6/-6	
106	AL132954	3	88997	T26I12	470883	4721	4726	IND	2	4/-4	
106	AL132954	3	88997	T26I12	470884	4886	4890	IND	2	3/-3	
106	AL132954	3	88997	T26I12	470885	63280	63286	IND	2	5/-5	
106	AL132954	3	88997	T26I12	470886	66768	66769	IND	2	-60/60	
106	AL132954	3	88997	T26I12	471555	27635	27636	IND	1	-1/1	
106	AL132954	3	88997	T26I12	471556	4727	4732	IND	1	4/-4	
106	AL132954	3	88997	T26I12	471557	4891	4895	IND	1	3/-3	
106	AL132954	3	88997	T26I12	471558	62259	62260	IND	1	-1/1	
106	AL132954	3	88997	T26I12	471559	65708	65709	IND	1	-1/1	
106	AL132954	3	88997	T26I12	471560	87497	87498	IND	1	-1/1	
107	AL132975	3	103240	T22E16	466802	5085	5087	SNP	1		C/A
107	AL132975	3	103240	T22E16	466803	5345	5347	SNP	1		C/A
107	AL132975	3	103240	T22E16	466804	5153	5155	SNP	1		G/C
107	AL132975	3	103240	T22E16	466805	5001	5003	SNP	1		A/C
107	AL132975	3	103240	T22E16	466806	5156	5158	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
107	AL132975	3	103240	T22E16	466807	5125	5127	SNP	1		T/G
107	AL132975	3	103240	T22E16	466808	5117	5119	SNP	1		A/G
107	AL132975	3	103240	T22E16	466932	89246	89248	SNP	1		C/T
107	AL132975	3	103240	T22E16	467013	21898	21900	SNP	1		T/A
107	AL132975	3	103240	T22E16	467014	22004	22006	SNP	1		T/C
107	AL132975	3	103240	T22E16	467015	21992	21994	SNP	1		A/C
107	AL132975	3	103240	T22E16	467016	21983	21985	SNP	1		T/C
107	AL132975	3	103240	T22E16	467017	21972	21974	SNP	1		T/C
107	AL132975	3	103240	T22E16	467018	21748	21750	SNP	1		A/G
107	AL132975	3	103240	T22E16	467019	22032	22034	SNP	1		A/G
107	AL132975	3	103240	T22E16	467020	21907	21909	SNP	1		C/T
107	AL132975	3	103240	T22E16	467155	33035	33037	SNP	1		T/A
107	AL132975	3	103240	T22E16	467156	32557	32559	SNP	1		C/A
107	AL132975	3	103240	T22E16	467227	11076	11078	SNP	1		G/A
107	AL132975	3	103240	T22E16	467355	27964	27966	SNP	1		T/C
107	AL132975	3	103240	T22E16	467413	100025	100027	SNP	1		G/A
107	AL132975	3	103240	T22E16	467414	100897	100899	SNP	1		T/C
107	AL132975	3	103240	T22E16	467415	101618	101620	SNP	1		A/C
107	AL132975	3	103240	T22E16	467416	99905	99907	SNP	1		C/G
107	AL132975	3	103240	T22E16	467417	101098	101100	SNP	1		C/T
107	AL132975	3	103240	T22E16	467585	27399	27401	SNP	1		C/T
107	AL132975	3	103240	T22E16	467820	81864	81866	SNP	1		A/G
107	AL132975	3	103240	T22E16	467858	65701	65703	SNP	1		C/T
107	AL132975	3	103240	T22E16	468079	30284	30286	SNP	1		G/A
107	AL132975	3	103240	T22E16	468080	30322	30324	SNP	1		G/A
107	AL132975	3	103240	T22E16	468081	30575	30577	SNP	1		T/A
107	AL132975	3	103240	T22E16	468082	30546	30548	SNP	1		T/C
107	AL132975	3	103240	T22E16	468083	30386	30388	SNP	1		A/T
107	AL132975	3	103240	T22E16	468084	30387	30389	SNP	1		A/T
107	AL132975	3	103240	T22E16	468318	98244	98246	SNP	1		T/A
107	AL132975	3	103240	T22E16	468319	99049	99051	SNP	1		T/A
107	AL132975	3	103240	T22E16	468320	98761	98763	SNP	1		T/C
107	AL132975	3	103240	T22E16	468321	98142	98144	SNP	1		C/T
107	AL132975	3	103240	T22E16	468381	53652	53654	SNP	1		C/G
107	AL132975	3	103240	T22E16	468382	85892	85894	SNP	1		C/T
107	AL132975	3	103240	T22E16	468448	37303	37305	SNP	1		C/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
107	AL132975	3	103240	T22E16	468706	33612	33614	SNP	1		G/A
107	AL132975	3	103240	T22E16	468810	50677	50679	SNP	1		T/C
107	AL132975	3	103240	T22E16	468811	50734	50736	SNP	1		A/G
107	AL132975	3	103240	T22E16	469086	14984	14986	SNP	1		A/C
107	AL132975	3	103240	T22E16	469311	83502	83504	SNP	1		T/C
107	AL132975	3	103240	T22E16	469312	83602	83604	SNP	1		A/G
107	AL132975	3	103240	T22E16	469321	43885	43887	SNP	1		T/A
107	AL132975	3	103240	T22E16	469322	44085	44087	SNP	1		A/G
107	AL132975	3	103240	T22E16	469393	3286	3288	SNP	1		G/A
107	AL132975	3	103240	T22E16	469394	3482	3484	SNP	1		C/A
107	AL132975	3	103240	T22E16	469395	3801	3803	SNP	1		G/T
107	AL132975	3	103240	T22E16	469457	51517	51519	SNP	1		G/T
107	AL132975	3	103240	T22E16	470793	102509	102522	IND	2	12/-12	
107	AL132975	3	103240	T22E16	470794	15415	15419	IND	2	3/-3	
107	AL132975	3	103240	T22E16	470795	23184	23206	IND	2	21/-21	
107	AL132975	3	103240	T22E16	470796	31085	31098	IND	2	12/-12	
107	AL132975	3	103240	T22E16	470797	39633	39643	IND	2	9/-9	
107	AL132975	3	103240	T22E16	470798	42041	42042	IND	2	-64/64	
107	AL132975	3	103240	T22E16	470799	43592	43599	IND	2	6/-6	
107	AL132975	3	103240	T22E16	470800	53704	53705	IND	2	-16/16	
107	AL132975	3	103240	T22E16	470801	57483	57497	IND	2	13/-13	
107	AL132975	3	103240	T22E16	470802	60200	60208	IND	2	7/-7	
107	AL132975	3	103240	T22E16	470803	60298	60299	IND	2	-6/6	
107	AL132975	3	103240	T22E16	470804	60299	60300	IND	2	-6/6	
107	AL132975	3	103240	T22E16	470805	60862	60885	IND	2	22/-22	
107	AL132975	3	103240	T22E16	470806	60960	60961	IND	2	-10/10	
107	AL132975	3	103240	T22E16	470807	60962	60963	IND	2	-10/10	
107	AL132975	3	103240	T22E16	470808	61413	61422	IND	2	8/-8	
107	AL132975	3	103240	T22E16	470809	64582	64586	IND	2	3/-3	
107	AL132975	3	103240	T22E16	470810	72342	72346	IND	2	3/-3	
107	AL132975	3	103240	T22E16	470811	74816	74821	IND	2	4/-4	
107	AL132975	3	103240	T22E16	470812	93774	93775	IND	2	-17/17	
107	AL132975	3	103240	T22E16	470813	99879	99880	IND	2	-3/3	
107	AL132975	3	103240	T22E16	471518	15421	15425	IND	1	3/-3	
107	AL132975	3	103240	T22E16	471519	30355	30357	IND	1	1/-1	
107	AL132975	3	103240	T22E16	471520	33720	33721	IND	1	-1/1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
107	AL132975	3	103240	T22E16	471521	53595	53597	IND	1	1/-1	
107	AL132975	3	103240	T22E16	471522	98798	98799	IND	1	-1/1	
107	AL132975	3	103240	T22E16	471523	99880	99881	IND	1	-3/3	
108	AL137080	3	85710	F28O9	472053	84225	84227	SNP	1		T/A
108	AL137080	3	85710	F28O9	472054	84083	84085	SNP	1		G/C
108	AL137080	3	85710	F28O9	472076	63736	63738	SNP	1		C/A
108	AL137080	3	85710	F28O9	472077	63878	63880	SNP	1		G/A
108	AL137080	3	85710	F28O9	472078	64340	64342	SNP	1		C/A
108	AL137080	3	85710	F28O9	472079	64367	64369	SNP	1		T/G
108	AL137080	3	85710	F28O9	472080	64369	64371	SNP	1		A/G
108	AL137080	3	85710	F28O9	472081	64430	64432	SNP	1		T/G
108	AL137080	3	85710	F28O9	472082	64431	64433	SNP	1		A/G
108	AL137080	3	85710	F28O9	472083	63961	63963	SNP	1		A/T
108	AL137080	3	85710	F28O9	472084	64186	64188	SNP	1		G/T
108	AL137080	3	85710	F28O9	472085	64272	64274	SNP	1		C/T
108	AL137080	3	85710	F28O9	472188	34475	34477	SNP	1		A/G
108	AL137080	3	85710	F28O9	472189	33763	33765	SNP	1		T/A
108	AL137080	3	85710	F28O9	472202	55881	55883	SNP	1		A/G
108	AL137080	3	85710	F28O9	472203	56890	56892	SNP	1		T/A
108	AL137080	3	85710	F28O9	472204	56963	56965	SNP	1		A/C
108	AL137080	3	85710	F28O9	472205	56896	56898	SNP	1		T/C
108	AL137080	3	85710	F28O9	472206	56956	56958	SNP	1		C/T
108	AL137080	3	85710	F28O9	472620	67610	67612	SNP	1		T/A
108	AL137080	3	85710	F28O9	472621	66114	66116	SNP	1		A/C
108	AL137080	3	85710	F28O9	472622	67154	67156	SNP	1		A/C
108	AL137080	3	85710	F28O9	472623	66090	66092	SNP	1		C/T
108	AL137080	3	85710	F28O9	472624	67222	67224	SNP	1		C/T
108	AL137080	3	85710	F28O9	472644	13254	13256	SNP	1		C/A
108	AL137080	3	85710	F28O9	472645	12379	12381	SNP	1		T/C
108	AL137080	3	85710	F28O9	472646	11997	11999	SNP	1		C/G
108	AL137080	3	85710	F28O9	472647	13568	13570	SNP	1		A/G
108	AL137080	3	85710	F28O9	472648	13142	13144	SNP	1		C/G
108	AL137080	3	85710	F28O9	472649	12230	12232	SNP	1		A/T
108	AL137080	3	85710	F28O9	472650	12030	12032	SNP	1		G/T
108	AL137080	3	85710	F28O9	472651	13600	13602	SNP	1		G/T
108	AL137080	3	85710	F28O9	472652	13260	13262	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
108	AL137080	3	85710	F28O9	472763	47340	47342	SNP	1		C/A
108	AL137080	3	85710	F28O9	472869	51448	51450	SNP	1		C/A
108	AL137080	3	85710	F28O9	472927	73343	73345	SNP	1		T/C
108	AL137080	3	85710	F28O9	472928	73611	73613	SNP	1		A/T
108	AL137080	3	85710	F28O9	473117	11554	11556	SNP	1		T/C
108	AL137080	3	85710	F28O9	473281	48964	48966	SNP	1		T/C
108	AL137080	3	85710	F28O9	473282	48214	48216	SNP	1		T/G
108	AL137080	3	85710	F28O9	473283	48196	48198	SNP	1		A/T
108	AL137080	3	85710	F28O9	473436	3346	3348	SNP	1		C/A
108	AL137080	3	85710	F28O9	473437	2889	2891	SNP	1		T/C
108	AL137080	3	85710	F28O9	473438	2288	2290	SNP	1		G/C
108	AL137080	3	85710	F28O9	473439	4691	4693	SNP	1		C/T
108	AL137080	3	85710	F28O9	473512	78082	78084	SNP	1		A/G
108	AL137080	3	85710	F28O9	473613	82151	82153	SNP	1		T/A
108	AL137080	3	85710	F28O9	473614	81749	81751	SNP	1		C/T
108	AL137080	3	85710	F28O9	473761	17775	17777	SNP	1		C/T
108	AL137080	3	85710	F28O9	473777	68826	68828	SNP	1		C/G
108	AL137080	3	85710	F28O9	473778	68866	68868	SNP	1		A/G
108	AL137080	3	85710	F28O9	473779	68817	68819	SNP	1		T/G
108	AL137080	3	85710	F28O9	473780	69581	69583	SNP	1		C/A
108	AL137080	3	85710	F28O9	473781	70006	70008	SNP	1		C/A
108	AL137080	3	85710	F28O9	473782	69589	69591	SNP	1		A/C
108	AL137080	3	85710	F28O9	473783	69583	69585	SNP	1		T/G
108	AL137080	3	85710	F28O9	473784	69661	69663	SNP	1		C/T
108	AL137080	3	85710	F28O9	473785	69967	69969	SNP	1		G/T
108	AL137080	3	85710	F28O9	473786	70015	70017	SNP	1		G/T
108	AL137080	3	85710	F28O9	473787	69591	69593	SNP	1		C/T
108	AL137080	3	85710	F28O9	473891	23228	23229	IND	2	-3/3	
108	AL137080	3	85710	F28O9	473892	25601	26078	IND	2	476/-476	
108	AL137080	3	85710	F28O9	473893	58122	58130	IND	2	7/-7	
108	AL137080	3	85710	F28O9	473894	58262	58263	IND	2	-12/12	
108	AL137080	3	85710	F28O9	473895	67581	67582	IND	2	-6/6	
108	AL137080	3	85710	F28O9	473896	69245	69250	IND	2	4/-4	
108	AL137080	3	85710	F28O9	473897	78603	78604	IND	2	-6/6	
108	AL137080	3	85710	F28O9	473898	79828	79833	IND	2	4/-4	
108	AL137080	3	85710	F28O9	474202	13257	13261	IND	1	3/-3	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
108	AL137080	3	85710	F28O9	474203	13262	13265	IND	1	2/-2	
108	AL137080	3	85710	F28O9	474204	13264	13266	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474205	17448	17449	IND	1	-2/2	
108	AL137080	3	85710	F28O9	474206	34186	34188	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474207	42972	42974	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474208	48448	48450	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474209	48974	48976	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474210	56923	56924	IND	1	-1/1	
108	AL137080	3	85710	F28O9	474211	56929	56931	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474212	57009	57011	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474213	65570	65571	IND	1	-1/1	
108	AL137080	3	85710	F28O9	474214	67584	67585	IND	1	-1/1	
108	AL137080	3	85710	F28O9	474215	67585	67586	IND	1	-5/5	
108	AL137080	3	85710	F28O9	474216	69694	69696	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474217	73585	73587	IND	1	1/-1	
108	AL137080	3	85710	F28O9	474218	78602	78603	IND	1	-2/2	
108	AL137080	3	85710	F28O9	474219	84228	84229	IND	1	-1/1	
109	AL133248	3	87503	T8H10	466886	54788	54790	SNP	1		A/G
109	AL133248	3	87503	T8H10	466887	56628	56630	SNP	1		C/T
109	AL133248	3	87503	T8H10	466888	56765	56767	SNP	1		G/T
109	AL133248	3	87503	T8H10	467105	16942	16944	SNP	1		T/C
109	AL133248	3	87503	T8H10	467106	16902	16904	SNP	1		T/G
109	AL133248	3	87503	T8H10	467107	16928	16930	SNP	1		T/G
109	AL133248	3	87503	T8H10	467108	16904	16906	SNP	1		A/T
109	AL133248	3	87503	T8H10	467109	23456	23458	SNP	1		C/A
109	AL133248	3	87503	T8H10	467110	23506	23508	SNP	1		G/A
109	AL133248	3	87503	T8H10	467111	23341	23343	SNP	1		A/G
109	AL133248	3	87503	T8H10	467112	24328	24330	SNP	1		C/A
109	AL133248	3	87503	T8H10	467113	24682	24684	SNP	1		T/G
109	AL133248	3	87503	T8H10	467228	77121	77123	SNP	1		A/T
109	AL133248	3	87503	T8H10	467411	10334	10336	SNP	1		A/G
109	AL133248	3	87503	T8H10	467702	15200	15202	SNP	1		A/C
109	AL133248	3	87503	T8H10	467839	68147	68149	SNP	1		A/C
109	AL133248	3	87503	T8H10	467955	45988	45990	SNP	1		A/G
109	AL133248	3	87503	T8H10	468230	64252	64254	SNP	1		T/C
109	AL133248	3	87503	T8H10	468231	64413	64415	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
109	AL133248	3	87503	T8H10	468261	13774	13776	SNP	1		C/T
109	AL133248	3	87503	T8H10	468714	59424	59426	SNP	1		C/T
109	AL133248	3	87503	T8H10	468715	59325	59327	SNP	1		A/T
109	AL133248	3	87503	T8H10	469336	85766	85768	SNP	1		G/A
109	AL133248	3	87503	T8H10	469337	85734	85736	SNP	1		T/G
109	AL133248	3	87503	T8H10	469338	85505	85507	SNP	1		A/T
109	AL133248	3	87503	T8H10	469339	85676	85678	SNP	1		C/T
109	AL133248	3	87503	T8H10	469403	30099	30101	SNP	1		G/A
109	AL133248	3	87503	T8H10	469404	30092	30094	SNP	1		G/A
109	AL133248	3	87503	T8H10	469430	49987	49989	SNP	1		C/G
109	AL133248	3	87503	T8H10	469431	49831	49833	SNP	1		A/T
109	AL133248	3	87503	T8H10	471032	28158	28159	IND	2	-4/4	
109	AL133248	3	87503	T8H10	471033	30318	30319	IND	2	-7/7	
109	AL133248	3	87503	T8H10	471034	55860	55861	IND	2	-4/4	
109	AL133248	3	87503	T8H10	471035	56784	56788	IND	2	3/-3	
109	AL133248	3	87503	T8H10	471036	57256	57267	IND	2	10/-10	
109	AL133248	3	87503	T8H10	471037	59517	59518	IND	2	-4/4	
109	AL133248	3	87503	T8H10	471038	63163	63164	IND	2	-9/9	
109	AL133248	3	87503	T8H10	471039	66314	66315	IND	2	-4/4	
109	AL133248	3	87503	T8H10	471040	73951	73952	IND	2	-6/6	
109	AL133248	3	87503	T8H10	471041	75798	75810	IND	2	11/-11	
109	AL133248	3	87503	T8H10	471614	16899	16900	IND	1	-2/2	
109	AL133248	3	87503	T8H10	471615	29965	29967	IND	1	1/-1	
109	AL133248	3	87503	T8H10	471616	40486	40487	IND	1	-1/1	
109	AL133248	3	87503	T8H10	471617	40488	40489	IND	1	-1/1	
109	AL133248	3	87503	T8H10	471618	56784	56786	IND	1	1/-1	
109	AL133248	3	87503	T8H10	471619	56786	56788	IND	1	1/-1	
109	AL133248	3	87503	T8H10	471620	56788	56790	IND	1	1/-1	
109	AL133248	3	87503	T8H10	471621	66332	66333	IND	1	-2/2	
110	AL132977	3	109016	T10K17	467534	108182	108184	SNP	1		A/C
110	AL132977	3	109016	T10K17	468299	32786	32788	SNP	1		C/A
110	AL132977	3	109016	T10K17	468300	32634	32636	SNP	1		T/C
110	AL132977	3	109016	T10K17	468301	32966	32968	SNP	1		G/C
110	AL132977	3	109016	T10K17	468302	32739	32741	SNP	1		C/T
110	AL132977	3	109016	T10K17	468303	32884	32886	SNP	1		C/T
110	AL132977	3	109016	T10K17	468735	60142	60144	SNP	1		A/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
110	AL132977	3	109016	T10K17	468879	102180	102182	SNP	1		A/T
110	AL132977	3	109016	T10K17	470547	17453	19003	IND	2	1549/-1549	
110	AL132977	3	109016	T10K17	470548	17468	19018	IND	2	1549/-1549	
110	AL132977	3	109016	T10K17	470549	18775	18783	IND	2	7/-7	
110	AL132977	3	109016	T10K17	470550	31427	31428	IND	2	-3/3	
110	AL132977	3	109016	T10K17	470551	39594	39595	IND	2	-70/70	
110	AL132977	3	109016	T10K17	471416	32623	32624	IND	1	-1/1	
111	AL137081	3	105306	F9D24	472581	11345	11347	SNP	1		A/C
112	AL137082	3	94239	F14P22	472390	66978	66980	SNP	1		T/C
112	AL137082	3	94239	F14P22	473194	22553	22555	SNP	1		A/T
112	AL137082	3	94239	F14P22	473270	79390	79392	SNP	1		T/A
112	AL137082	3	94239	F14P22	473413	33179	33181	SNP	1		T/C
112	AL137082	3	94239	F14P22	473414	33375	33377	SNP	1		A/G
113	AL138659	3	91851	T16L24	471682	57129	57131	SNP	1		T/C
113	AL138659	3	91851	T16L24	471746	59850	59852	SNP	1		T/C
113	AL138659	3	91851	T16L24	471872	25320	25322	SNP	1		G/A
113	AL138659	3	91851	T16L24	471873	23227	23229	SNP	1		C/A
113	AL138659	3	91851	T16L24	471874	23548	23550	SNP	1		G/T
113	AL138659	3	91851	T16L24	472109	10281	10283	SNP	1		G/A
113	AL138659	3	91851	T16L24	472110	9793	9795	SNP	1		G/A
113	AL138659	3	91851	T16L24	472111	11112	11114	SNP	1		C/A
113	AL138659	3	91851	T16L24	472112	10588	10590	SNP	1		T/C
113	AL138659	3	91851	T16L24	472113	9840	9842	SNP	1		A/T
113	AL138659	3	91851	T16L24	472114	10968	10970	SNP	1		A/T
113	AL138659	3	91851	T16L24	472115	11274	11276	SNP	1		C/T
113	AL138659	3	91851	T16L24	472336	30259	30261	SNP	1		A/C
113	AL138659	3	91851	T16L24	472337	30488	30490	SNP	1		C/G
113	AL138659	3	91851	T16L24	472768	60777	60779	SNP	1		G/A
113	AL138659	3	91851	T16L24	472769	61791	61793	SNP	1		A/C
113	AL138659	3	91851	T16L24	472770	61790	61792	SNP	1		A/C
113	AL138659	3	91851	T16L24	472771	61566	61568	SNP	1		C/T
113	AL138659	3	91851	T16L24	472885	50452	50454	SNP	1		T/C
113	AL138659	3	91851	T16L24	472924	12278	12280	SNP	1		T/C
113	AL138659	3	91851	T16L24	472925	12380	12382	SNP	1		A/T
113	AL138659	3	91851	T16L24	472929	32368	32370	SNP	1		T/C
113	AL138659	3	91851	T16L24	472930	32490	32492	SNP	1		G/C

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113	AL138659	3	91851	T16L24	472931	31619	31621	SNP	1		G/C
113	AL138659	3	91851	T16L24	472933	1440	1442	SNP	1		G/A
113	AL138659	3	91851	T16L24	472934	1554	1556	SNP	1		C/G
113	AL138659	3	91851	T16L24	473014	43824	43826	SNP	1		T/A
113	AL138659	3	91851	T16L24	473015	43646	43648	SNP	1		T/C
113	AL138659	3	91851	T16L24	473016	36806	36808	SNP	1		C/A
113	AL138659	3	91851	T16L24	473017	36749	36751	SNP	1		C/A
113	AL138659	3	91851	T16L24	473408	66803	66805	SNP	1		T/A
113	AL138659	3	91851	T16L24	473409	66291	66293	SNP	1		G/C
113	AL138659	3	91851	T16L24	473410	64916	64918	SNP	1		C/G
113	AL138659	3	91851	T16L24	473411	65536	65538	SNP	1		C/T
113	AL138659	3	91851	T16L24	473445	62592	62594	SNP	1		A/T
113	AL138659	3	91851	T16L24	473637	59041	59043	SNP	1		T/A
113	AL138659	3	91851	T16L24	473638	58947	58949	SNP	1		T/C
113	AL138659	3	91851	T16L24	474001	122	123	IND	2	-5/5	
113	AL138659	3	91851	T16L24	474002	2393	2394	IND	2	-10/10	
113	AL138659	3	91851	T16L24	474003	347	351	IND	2	3/-3	
113	AL138659	3	91851	T16L24	474004	4121	4122	IND	2	-7/7	
113	AL138659	3	91851	T16L24	474398	11222	11223	IND	1	-1/1	
113	AL138659	3	91851	T16L24	474399	11279	11280	IND	1	-2/2	
113	AL138659	3	91851	T16L24	474400	25207	25208	IND	1	-6/6	
113	AL138659	3	91851	T16L24	474401	25544	25546	IND	1	1/-1	
113	AL138659	3	91851	T16L24	474402	25611	25612	IND	1	-1/1	
113	AL138659	3	91851	T16L24	474403	44217	44218	IND	1	-1/1	
113	AL138659	3	91851	T16L24	474404	61754	61756	IND	1	1/-1	
113	AL138659	3	91851	T16L24	474405	65506	65508	IND	1	1/-1	
113	AL138659	3	91851	T16L24	474406	66385	66387	IND	1	1/-1	
114	AL137898	3	109155	T20K12	471744	44654	44656	SNP	1		C/T
114	AL137898	3	109155	T20K12	472055	91104	91106	SNP	1		G/A
114	AL137898	3	109155	T20K12	472056	91396	91398	SNP	1		A/G
114	AL137898	3	109155	T20K12	472069	71286	71288	SNP	1		T/G
114	AL137898	3	109155	T20K12	472227	26254	26256	SNP	1		A/G
114	AL137898	3	109155	T20K12	472230	21189	21191	SNP	1		G/A
114	AL137898	3	109155	T20K12	472231	21162	21164	SNP	1		C/A
114	AL137898	3	109155	T20K12	472232	21143	21145	SNP	1		G/C
114	AL137898	3	109155	T20K12	472233	21188	21190	SNP	1		A/G

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114	AL137898	3	109155	T20K12	472234	21175	21177	SNP	1		C/T
114	AL137898	3	109155	T20K12	472346	90221	90223	SNP	1		A/C
114	AL137898	3	109155	T20K12	472376	81292	81294	SNP	1		A/T
114	AL137898	3	109155	T20K12	472536	13315	13317	SNP	1		A/C
114	AL137898	3	109155	T20K12	472537	13295	13297	SNP	1		T/C
114	AL137898	3	109155	T20K12	472538	13576	13578	SNP	1		A/G
114	AL137898	3	109155	T20K12	472539	13329	13331	SNP	1		A/G
114	AL137898	3	109155	T20K12	472540	13537	13539	SNP	1		C/T
114	AL137898	3	109155	T20K12	472678	65821	65823	SNP	1		A/C
114	AL137898	3	109155	T20K12	472727	36927	36929	SNP	1		A/C
114	AL137898	3	109155	T20K12	472728	37186	37188	SNP	1		A/T
114	AL137898	3	109155	T20K12	472729	35691	35693	SNP	1		T/A
114	AL137898	3	109155	T20K12	472730	36429	36431	SNP	1		G/T
114	AL137898	3	109155	T20K12	472731	35961	35963	SNP	1		C/T
114	AL137898	3	109155	T20K12	472732	36486	36488	SNP	1		C/T
114	AL137898	3	109155	T20K12	472897	72533	72535	SNP	1		G/A
114	AL137898	3	109155	T20K12	472898	72046	72048	SNP	1		A/C
114	AL137898	3	109155	T20K12	472899	72199	72201	SNP	1		T/C
114	AL137898	3	109155	T20K12	472900	72393	72395	SNP	1		T/C
114	AL137898	3	109155	T20K12	473025	67307	67309	SNP	1		G/A
114	AL137898	3	109155	T20K12	473026	67306	67308	SNP	1		A/C
114	AL137898	3	109155	T20K12	473027	67242	67244	SNP	1		A/G
114	AL137898	3	109155	T20K12	473387	64427	64429	SNP	1		A/C
114	AL137898	3	109155	T20K12	473388	64428	64430	SNP	1		A/T
114	AL137898	3	109155	T20K12	473428	29387	29389	SNP	1		T/C
114	AL137898	3	109155	T20K12	473429	29270	29272	SNP	1		A/C
114	AL137898	3	109155	T20K12	473430	29545	29547	SNP	1		T/C
114	AL137898	3	109155	T20K12	473431	29243	29245	SNP	1		C/G
114	AL137898	3	109155	T20K12	473432	30245	30247	SNP	1		C/T
114	AL137898	3	109155	T20K12	473451	69139	69141	SNP	1		A/T
114	AL137898	3	109155	T20K12	473452	69138	69140	SNP	1		A/T
114	AL137898	3	109155	T20K12	473505	23110	23112	SNP	1		A/T
114	AL137898	3	109155	T20K12	473607	76364	76366	SNP	1		T/A
114	AL137898	3	109155	T20K12	473608	76231	76233	SNP	1		T/C
114	AL137898	3	109155	T20K12	473609	76360	76362	SNP	1		G/C
114	AL137898	3	109155	T20K12	473610	77568	77570	SNP	1		A/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
114	AL137898	3	109155	T20K12	473611	76328	76330	SNP	1		A/T
114	AL137898	3	109155	T20K12	473612	76388	76390	SNP	1		C/T
114	AL137898	3	109155	T20K12	473618	94153	94155	SNP	1		A/C
114	AL137898	3	109155	T20K12	473619	94133	94135	SNP	1		C/T
114	AL137898	3	109155	T20K12	473650	33568	33570	SNP	1		A/G
114	AL137898	3	109155	T20K12	473746	24470	24472	SNP	1		A/T
114	AL137898	3	109155	T20K12	473747	24547	24549	SNP	1		C/T
114	AL137898	3	109155	T20K12	473763	52382	52384	SNP	1		G/A
114	AL137898	3	109155	T20K12	474017	2227	2228	IND	2	-9/9	
114	AL137898	3	109155	T20K12	474018	2301	2326	IND	2	24/-24	
114	AL137898	3	109155	T20K12	474421	13776	13778	IND	1	1/-1	
114	AL137898	3	109155	T20K12	474422	13778	13780	IND	1	1/-1	
114	AL137898	3	109155	T20K12	474423	21196	21197	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474424	24251	24252	IND	1	-4/4	
114	AL137898	3	109155	T20K12	474425	24427	24428	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474426	24492	24494	IND	1	1/-1	
114	AL137898	3	109155	T20K12	474427	26418	26419	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474428	29644	29645	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474429	36101	36102	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474430	52679	52680	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474431	68863	68864	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474432	69142	69144	IND	1	1/-1	
114	AL137898	3	109155	T20K12	474433	72268	72269	IND	1	-1/1	
114	AL137898	3	109155	T20K12	474434	91118	91119	IND	1	-2/2	
115	AL132962	3	95993	F2A19	466792	34219	34221	SNP	1		T/A
115	AL132962	3	95993	F2A19	466793	35343	35345	SNP	1		T/C
115	AL132962	3	95993	F2A19	466794	35244	35246	SNP	1		G/C
115	AL132962	3	95993	F2A19	466795	34482	34484	SNP	1		A/G
115	AL132962	3	95993	F2A19	466796	35375	35377	SNP	1		A/G
115	AL132962	3	95993	F2A19	466955	30405	30407	SNP	1		G/A
115	AL132962	3	95993	F2A19	466956	30570	30572	SNP	1		T/A
115	AL132962	3	95993	F2A19	467349	80164	80166	SNP	1		C/G
115	AL132962	3	95993	F2A19	467394	10918	10920	SNP	1		C/G
115	AL132962	3	95993	F2A19	467395	10935	10937	SNP	1		C/T
115	AL132962	3	95993	F2A19	467498	88667	88669	SNP	1		C/A
115	AL132962	3	95993	F2A19	467586	23929	23931	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
115	AL132962	3	95993	F2A19	467681	42658	42660	SNP	1		C/G
115	AL132962	3	95993	F2A19	467795	13717	13719	SNP	1		T/A
115	AL132962	3	95993	F2A19	467796	13700	13702	SNP	1		A/T
115	AL132962	3	95993	F2A19	467797	13735	13737	SNP	1		A/T
115	AL132962	3	95993	F2A19	467798	13741	13743	SNP	1		A/T
115	AL132962	3	95993	F2A19	468092	23139	23141	SNP	1		C/G
115	AL132962	3	95993	F2A19	468114	43683	43685	SNP	1		G/A
115	AL132962	3	95993	F2A19	468115	43639	43641	SNP	1		T/G
115	AL132962	3	95993	F2A19	468116	43570	43572	SNP	1		G/T
115	AL132962	3	95993	F2A19	468359	49654	49656	SNP	1		G/T
115	AL132962	3	95993	F2A19	468396	38745	38747	SNP	1		A/T
115	AL132962	3	95993	F2A19	468397	38753	38755	SNP	1		G/T
115	AL132962	3	95993	F2A19	468544	72108	72110	SNP	1		G/A
115	AL132962	3	95993	F2A19	468545	71949	71951	SNP	1		A/C
115	AL132962	3	95993	F2A19	468546	72676	72678	SNP	1		T/C
115	AL132962	3	95993	F2A19	468547	72470	72472	SNP	1		G/C
115	AL132962	3	95993	F2A19	468548	72729	72731	SNP	1		A/T
115	AL132962	3	95993	F2A19	468549	72666	72668	SNP	1		A/T
115	AL132962	3	95993	F2A19	468550	72665	72667	SNP	1		A/T
115	AL132962	3	95993	F2A19	468687	19792	19794	SNP	1		T/A
115	AL132962	3	95993	F2A19	468688	19643	19645	SNP	1		G/A
115	AL132962	3	95993	F2A19	468689	19659	19661	SNP	1		T/A
115	AL132962	3	95993	F2A19	468690	19606	19608	SNP	1		T/G
115	AL132962	3	95993	F2A19	468691	20050	20052	SNP	1		A/G
115	AL132962	3	95993	F2A19	468692	19802	19804	SNP	1		C/T
115	AL132962	3	95993	F2A19	468693	19807	19809	SNP	1		A/T
115	AL132962	3	95993	F2A19	468694	19658	19660	SNP	1		A/T
115	AL132962	3	95993	F2A19	468708	56558	56560	SNP	1		G/T
115	AL132962	3	95993	F2A19	468824	90836	90838	SNP	1		G/A
115	AL132962	3	95993	F2A19	468825	90562	90564	SNP	1		G/A
115	AL132962	3	95993	F2A19	468826	90015	90017	SNP	1		C/A
115	AL132962	3	95993	F2A19	468827	90866	90868	SNP	1		T/C
115	AL132962	3	95993	F2A19	468828	89975	89977	SNP	1		T/C
115	AL132962	3	95993	F2A19	468829	90869	90871	SNP	1		A/G
115	AL132962	3	95993	F2A19	468830	90755	90757	SNP	1		C/G
115	AL132962	3	95993	F2A19	468831	90732	90734	SNP	1		C/G

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
115	AL132962	3	95993	F2A19	468832	90605	90607	SNP	1		A/T
115	AL132962	3	95993	F2A19	468833	90555	90557	SNP	1		A/T
115	AL132962	3	95993	F2A19	468834	89954	89956	SNP	1		C/T
115	AL132962	3	95993	F2A19	469076	4646	4648	SNP	1		G/A
115	AL132962	3	95993	F2A19	469077	4663	4665	SNP	1		C/T
115	AL132962	3	95993	F2A19	469178	75109	75111	SNP	1		T/C
115	AL132962	3	95993	F2A19	469179	74723	74725	SNP	1		C/T
115	AL132962	3	95993	F2A19	469265	30985	30987	SNP	1		C/T
115	AL132962	3	95993	F2A19	469432	15444	15446	SNP	1		T/C
115	AL132962	3	95993	F2A19	470104	10975	10976	IND	2	-4/4	
115	AL132962	3	95993	F2A19	470105	13302	13306	IND	2	3/-3	
115	AL132962	3	95993	F2A19	470106	17591	17592	IND	2	-7/7	
115	AL132962	3	95993	F2A19	470107	26441	26456	IND	2	14/-14	
115	AL132962	3	95993	F2A19	470108	32217	32218	IND	2	-13/13	
115	AL132962	3	95993	F2A19	470109	37319	37353	IND	2	33/-33	
115	AL132962	3	95993	F2A19	470110	37576	37580	IND	2	3/-3	
115	AL132962	3	95993	F2A19	470111	41138	41146	IND	2	7/-7	
115	AL132962	3	95993	F2A19	470112	43523	43530	IND	2	6/-6	
115	AL132962	3	95993	F2A19	470113	47701	47705	IND	2	3/-3	
115	AL132962	3	95993	F2A19	470114	52148	52149	IND	2	-3/3	
115	AL132962	3	95993	F2A19	470115	58489	58490	IND	2	-9/9	
115	AL132962	3	95993	F2A19	470116	65619	65624	IND	2	4/-4	
115	AL132962	3	95993	F2A19	470117	79229	79230	IND	2	-3/3	
115	AL132962	3	95993	F2A19	470118	89712	89713	IND	2	-3/3	
115	AL132962	3	95993	F2A19	471283	17592	17593	IND	1	-1/1	
115	AL132962	3	95993	F2A19	471284	17593	17594	IND	1	-3/3	
115	AL132962	3	95993	F2A19	471285	17597	17598	IND	1	-1/1	
115	AL132962	3	95993	F2A19	471286	19591	19593	IND	1	1/-1	
115	AL132962	3	95993	F2A19	471287	20539	20540	IND	1	-2/2	
115	AL132962	3	95993	F2A19	471288	35553	35554	IND	1	-1/1	
115	AL132962	3	95993	F2A19	471289	38530	38531	IND	1	-1/1	
115	AL132962	3	95993	F2A19	471290	38567	38570	IND	1	2/-2	
115	AL132962	3	95993	F2A19	471291	42508	42511	IND	1	2/-2	
115	AL132962	3	95993	F2A19	471292	43530	43533	IND	1	2/-2	
115	AL132962	3	95993	F2A19	471293	72646	72647	IND	1	-1/1	
115	AL132962	3	95993	F2A19	471294	72671	72673	IND	1	1/-1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
115	AL132962	3	95993	F2A19	471295	74948	74950	IND	1	1/-1	
115	AL132962	3	95993	F2A19	471296	80224	80227	IND	1	2/-2	
116	AL132959	3	104868	F15G16	466925	18922	18924	SNP	1		T/C
116	AL132959	3	104868	F15G16	466979	70637	70639	SNP	1		G/C
116	AL132959	3	104868	F15G16	466980	71010	71012	SNP	1		A/G
116	AL132959	3	104868	F15G16	467350	88907	88909	SNP	1		A/G
116	AL132959	3	104868	F15G16	468252	86417	86419	SNP	1		C/G
116	AL132959	3	104868	F15G16	468663	74318	74320	SNP	1		C/A
116	AL132959	3	104868	F15G16	468767	83378	83380	SNP	1		T/C
116	AL132959	3	104868	F15G16	468768	83919	83921	SNP	1		T/C
116	AL132959	3	104868	F15G16	468862	17703	17705	SNP	1		C/A
116	AL132959	3	104868	F15G16	468863	17702	17704	SNP	1		C/A
116	AL132959	3	104868	F15G16	468864	17820	17822	SNP	1		G/C
116	AL132959	3	104868	F15G16	469675	21118	21131	IND	2	12/-12	
116	AL132959	3	104868	F15G16	469676	68730	68731	IND	2	-5/5	
116	AL132959	3	104868	F15G16	469677	6931	6932	IND	2	-3/3	
116	AL132959	3	104868	F15G16	469678	71583	71602	IND	2	18/-18	
116	AL132959	3	104868	F15G16	469679	71608	71627	IND	2	18/-18	
116	AL132959	3	104868	F15G16	469680	77182	77369	IND	2	186/-186	
116	AL132959	3	104868	F15G16	469681	77898	77903	IND	2	4/-4	
116	AL132959	3	104868	F15G16	469682	78390	78410	IND	2	19/-19	
116	AL132959	3	104868	F15G16	469683	81277	81281	IND	2	3/-3	
116	AL132959	3	104868	F15G16	469684	82206	82207	IND	2	-6/6	
116	AL132959	3	104868	F15G16	469685	82208	82209	IND	2	-6/6	
116	AL132959	3	104868	F15G16	471148	23408	23410	IND	1	1/-1	
116	AL132959	3	104868	F15G16	471149	90772	90773	IND	1	-1/1	
116	AL132959	3	104868	F15G16	471150	97365	97366	IND	1	-1/1	
117	AL050399	4	80019	F25E4	471740	43051	43053	SNP	1		A/C
117	AL050399	4	80019	F25E4	471898	69555	69557	SNP	1		G/A
117	AL050399	4	80019	F25E4	471899	69551	69553	SNP	1		T/C
117	AL050399	4	80019	F25E4	471900	69949	69951	SNP	1		G/C
117	AL050399	4	80019	F25E4	471901	69735	69737	SNP	1		A/G
117	AL050399	4	80019	F25E4	471902	69879	69881	SNP	1		A/G
117	AL050399	4	80019	F25E4	471903	69952	69954	SNP	1		C/T
117	AL050399	4	80019	F25E4	471904	70031	70033	SNP	1		C/T
117	AL050399	4	80019	F25E4	471905	70110	70112	SNP	1		G/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
117	AL050399	4	80019	F25E4	472029	41866	41868	SNP	1		T/A
117	AL050399	4	80019	F25E4	472030	41613	41615	SNP	1		C/A
117	AL050399	4	80019	F25E4	472031	42204	42206	SNP	1		T/C
117	AL050399	4	80019	F25E4	472032	41640	41642	SNP	1		A/C
117	AL050399	4	80019	F25E4	472033	41616	41618	SNP	1		T/C
117	AL050399	4	80019	F25E4	472034	41607	41609	SNP	1		A/G
117	AL050399	4	80019	F25E4	472035	41673	41675	SNP	1		A/T
117	AL050399	4	80019	F25E4	472173	32245	32247	SNP	1		G/A
117	AL050399	4	80019	F25E4	472174	31023	31025	SNP	1		C/A
117	AL050399	4	80019	F25E4	472175	31024	31026	SNP	1		T/A
117	AL050399	4	80019	F25E4	472176	31025	31027	SNP	1		T/A
117	AL050399	4	80019	F25E4	472177	31026	31028	SNP	1		T/A
117	AL050399	4	80019	F25E4	472178	31027	31029	SNP	1		T/A
117	AL050399	4	80019	F25E4	472179	32569	32571	SNP	1		G/C
117	AL050399	4	80019	F25E4	472240	22948	22950	SNP	1		A/G
117	AL050399	4	80019	F25E4	473090	27338	27340	SNP	1		G/A
117	AL050399	4	80019	F25E4	473091	27435	27437	SNP	1		T/C
117	AL050399	4	80019	F25E4	473092	27519	27521	SNP	1		T/C
117	AL050399	4	80019	F25E4	473093	27642	27644	SNP	1		A/C
117	AL050399	4	80019	F25E4	473094	28544	28546	SNP	1		T/G
117	AL050399	4	80019	F25E4	473095	27640	27642	SNP	1		A/G
117	AL050399	4	80019	F25E4	473096	27641	27643	SNP	1		A/G
117	AL050399	4	80019	F25E4	473097	27643	27645	SNP	1		A/G
117	AL050399	4	80019	F25E4	473098	27532	27534	SNP	1		C/T
117	AL050399	4	80019	F25E4	473099	27644	27646	SNP	1		G/T
117	AL050399	4	80019	F25E4	473412	21102	21104	SNP	1		C/T
117	AL050399	4	80019	F25E4	474156	21845	21846	IND	1	-1/1	
117	AL050399	4	80019	F25E4	474157	27448	27450	IND	1	1/-1	
117	AL050399	4	80019	F25E4	474158	27644	27645	IND	1	-2/2	
117	AL050399	4	80019	F25E4	474159	27645	27646	IND	1	-1/1	
117	AL050399	4	80019	F25E4	474160	27646	27647	IND	1	-3/3	
118	AL137189	5	114759	F7J8	471656	24902	24904	SNP	1		A/T
118	AL137189	5	114759	F7J8	471709	10080	10082	SNP	1		A/T
118	AL137189	5	114759	F7J8	471710	10082	10084	SNP	1		A/T
118	AL137189	5	114759	F7J8	471718	82857	82859	SNP	1		T/C
118	AL137189	5	114759	F7J8	471719	82784	82786	SNP	1		C/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
118	AL137189	5	114759	F7J8	471754	11422	11424	SNP	1		G/C
118	AL137189	5	114759	F7J8	471760	91013	91015	SNP	1		T/C
118	AL137189	5	114759	F7J8	471761	91135	91137	SNP	1		A/G
118	AL137189	5	114759	F7J8	471762	90937	90939	SNP	1		C/T
118	AL137189	5	114759	F7J8	471763	90907	90909	SNP	1		C/T
118	AL137189	5	114759	F7J8	471764	90801	90803	SNP	1		C/T
118	AL137189	5	114759	F7J8	471847	48325	48327	SNP	1		T/C
118	AL137189	5	114759	F7J8	471947	47558	47560	SNP	1		C/A
118	AL137189	5	114759	F7J8	471948	47616	47618	SNP	1		A/G
118	AL137189	5	114759	F7J8	472042	21004	21006	SNP	1		G/A
118	AL137189	5	114759	F7J8	472043	21115	21117	SNP	1		A/G
118	AL137189	5	114759	F7J8	472157	81466	81468	SNP	1		A/T
118	AL137189	5	114759	F7J8	472218	52757	52759	SNP	1		A/G
118	AL137189	5	114759	F7J8	472219	52902	52904	SNP	1		C/G
118	AL137189	5	114759	F7J8	472228	89863	89865	SNP	1		T/A
118	AL137189	5	114759	F7J8	472229	90191	90193	SNP	1		C/T
118	AL137189	5	114759	F7J8	472272	101609	101611	SNP	1		A/T
118	AL137189	5	114759	F7J8	472479	16714	16716	SNP	1		T/A
118	AL137189	5	114759	F7J8	472480	14988	14990	SNP	1		C/G
118	AL137189	5	114759	F7J8	472481	14794	14796	SNP	1		C/T
118	AL137189	5	114759	F7J8	472662	55679	55681	SNP	1		G/C
118	AL137189	5	114759	F7J8	472711	63850	63852	SNP	1		T/A
118	AL137189	5	114759	F7J8	472712	64011	64013	SNP	1		A/G
118	AL137189	5	114759	F7J8	473100	96195	96197	SNP	1		A/T
118	AL137189	5	114759	F7J8	473101	96227	96229	SNP	1		C/T
118	AL137189	5	114759	F7J8	473253	103952	103954	SNP	1		T/A
118	AL137189	5	114759	F7J8	473254	103710	103712	SNP	1		C/A
118	AL137189	5	114759	F7J8	473255	104043	104045	SNP	1		T/C
118	AL137189	5	114759	F7J8	473256	103870	103872	SNP	1		T/C
118	AL137189	5	114759	F7J8	473257	103590	103592	SNP	1		C/G
118	AL137189	5	114759	F7J8	473260	89247	89249	SNP	1		G/A
118	AL137189	5	114759	F7J8	473261	88842	88844	SNP	1		G/A
118	AL137189	5	114759	F7J8	473262	88800	88802	SNP	1		G/A
118	AL137189	5	114759	F7J8	473263	89301	89303	SNP	1		A/C
118	AL137189	5	114759	F7J8	473264	89243	89245	SNP	1		C/G
118	AL137189	5	114759	F7J8	473265	88752	88754	SNP	1		A/T

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
118	AL137189	5	114759	F7J8	473274	23890	23892	SNP	1		G/A
118	AL137189	5	114759	F7J8	473349	84566	84568	SNP	1		G/T
118	AL137189	5	114759	F7J8	473453	49973	49975	SNP	1		C/G
118	AL137189	5	114759	F7J8	474279	104025	104026	IND	1	-1/1	
118	AL137189	5	114759	F7J8	474280	21300	21301	IND	1	-1/1	
118	AL137189	5	114759	F7J8	474281	80666	80668	IND	1	1/-1	
118	AL137189	5	114759	F7J8	474282	839	841	IND	1	1/-1	
118	AL137189	5	114759	F7J8	474283	88914	88916	IND	1	1/-1	
118	AL137189	5	114759	F7J8	474284	89465	89466	IND	1	-1/1	
118	AL137189	5	114759	F7J8	474285	89467	89468	IND	1	-1/1	
118	AL137189	5	114759	F7J8	474286	90825	90827	IND	1	1/-1	
118	AL137189	5	114759	F7J8	474287	91374	91376	IND	1	1/-1	
118	AL137189	5	114759	F7J8	474288	96727	96728	IND	1	-1/1	
118	AL137189	5	114759	F7J8	474289	99285	99287	IND	1	1/-1	
118	AL137189	5	114759	F7J8	474290	99301	99302	IND	1	-2/2	
119	AL133421	5	88095	F13G24	472436	84590	84592	SNP	1		G/T
119	AL133421	5	88095	F13G24	473138	67070	67072	SNP	1		T/A
119	AL133421	5	88095	F13G24	473139	68503	68505	SNP	1		T/A
119	AL133421	5	88095	F13G24	473140	68203	68205	SNP	1		T/C
119	AL133421	5	88095	F13G24	473141	68485	68487	SNP	1		T/C
119	AL133421	5	88095	F13G24	473142	68316	68318	SNP	1		A/G
119	AL133421	5	88095	F13G24	473143	68504	68506	SNP	1		A/T
119	AL133421	5	88095	F13G24	473377	78518	78520	SNP	1		C/A
119	AL133421	5	88095	F13G24	473378	78403	78405	SNP	1		A/C
119	AL133421	5	88095	F13G24	473379	78634	78636	SNP	1		G/C
119	AL133421	5	88095	F13G24	473380	78484	78486	SNP	1		A/G
119	AL133421	5	88095	F13G24	473381	78716	78718	SNP	1		C/G
119	AL133421	5	88095	F13G24	473382	78732	78734	SNP	1		A/G
119	AL133421	5	88095	F13G24	473383	78807	78809	SNP	1		A/G
119	AL133421	5	88095	F13G24	473384	79012	79014	SNP	1		T/G
119	AL133421	5	88095	F13G24	473385	78731	78733	SNP	1		C/T
119	AL133421	5	88095	F13G24	473661	77179	77181	SNP	1		T/A
119	AL133421	5	88095	F13G24	473662	77195	77197	SNP	1		G/A
119	AL133421	5	88095	F13G24	473663	77284	77286	SNP	1		T/A
119	AL133421	5	88095	F13G24	473664	77165	77167	SNP	1		A/C
119	AL133421	5	88095	F13G24	473665	77184	77186	SNP	1		T/C

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
119	AL133421	5	88095	F13G24	473666	77245	77247	SNP	1		G/C
119	AL133421	5	88095	F13G24	473667	77164	77166	SNP	1		A/G
119	AL133421	5	88095	F13G24	473668	77236	77238	SNP	1		C/G
119	AL133421	5	88095	F13G24	473669	77491	77493	SNP	1		A/G
119	AL133421	5	88095	F13G24	473670	76222	76224	SNP	1		T/G
119	AL133421	5	88095	F13G24	473671	77217	77219	SNP	1		C/T
119	AL133421	5	88095	F13G24	473672	77238	77240	SNP	1		A/T
119	AL133421	5	88095	F13G24	473814	1160	1161	IND	2	-3/3	
119	AL133421	5	88095	F13G24	473815	1161	1162	IND	2	-3/3	
119	AL133421	5	88095	F13G24	473816	1162	1163	IND	2	-3/3	
119	AL133421	5	88095	F13G24	473817	15261	15262	IND	2	-15/15	
119	AL133421	5	88095	F13G24	473818	15834	18367	IND	2	2532/-2532	
119	AL133421	5	88095	F13G24	473819	2802	2809	IND	2	6/-6	
119	AL133421	5	88095	F13G24	473820	8785	8801	IND	2	15/-15	
119	AL133421	5	88095	F13G24	474043	67283	67284	IND	1	-1/1	
119	AL133421	5	88095	F13G24	474044	77199	77201	IND	1	1/-1	
119	AL133421	5	88095	F13G24	474045	78406	78408	IND	1	1/-1	
119	AL133421	5	88095	F13G24	474046	78409	78412	IND	1	2/-2	
120	AC006601	5	110684	T14C9	471792	86400	86402	SNP	1		A/G
120	AC006601	5	110684	T14C9	471793	88768	88770	SNP	1		A/G
120	AC006601	5	110684	T14C9	471794	88913	88915	SNP	1		A/G
120	AC006601	5	110684	T14C9	471921	87986	87988	SNP	1		A/G
120	AC006601	5	110684	T14C9	471922	87991	87993	SNP	1		T/G
120	AC006601	5	110684	T14C9	471923	87992	87994	SNP	1		A/G
120	AC006601	5	110684	T14C9	471924	88039	88041	SNP	1		C/T
120	AC006601	5	110684	T14C9	471925	88048	88050	SNP	1		G/T
120	AC006601	5	110684	T14C9	472086	75170	75172	SNP	1		C/A
120	AC006601	5	110684	T14C9	472702	35407	35409	SNP	1		G/A
120	AC006601	5	110684	T14C9	472703	34927	34929	SNP	1		G/A
120	AC006601	5	110684	T14C9	473161	28268	28270	SNP	1		A/G
120	AC006601	5	110684	T14C9	473350	52670	52672	SNP	1		C/A
120	AC006601	5	110684	T14C9	473509	59067	59069	SNP	1		C/T
120	AC006601	5	110684	T14C9	473752	74033	74035	SNP	1		T/G
120	AC006601	5	110684	T14C9	474371	28101	28103	IND	1	1/-1	
120	AC006601	5	110684	T14C9	474372	29435	29437	IND	1	1/-1	
120	AC006601	5	110684	T14C9	474373	29480	29482	IND	1	1/-1	

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
120	AC006601	5	110684	T14C9	474374	86763	86765	IND	1	1/-1	
121	AC007627	5	157000	F15F15	466971	87040	87042	SNP	1		T/C
121	AC007627	5	157000	F15F15	466972	85824	85826	SNP	1		A/T
121	AC007627	5	157000	F15F15	466973	86844	86846	SNP	1		C/T
121	AC007627	5	157000	F15F15	467792	110731	110733	SNP	1		C/G
121	AC007627	5	157000	F15F15	467793	110763	110765	SNP	1		C/T
121	AC007627	5	157000	F15F15	467794	110923	110925	SNP	1		C/T
121	AC007627	5	157000	F15F15	469174	84896	84898	SNP	1		A/G
121	AC007627	5	157000	F15F15	469658	101610	101611	IND	2	-11/11	
121	AC007627	5	157000	F15F15	469659	102591	102611	IND	2	19/-19	
121	AC007627	5	157000	F15F15	469660	13919	13924	IND	2	4/-4	
121	AC007627	5	157000	F15F15	469661	14463	14468	IND	2	4/-4	
121	AC007627	5	157000	F15F15	469662	16216	16221	IND	2	4/-4	
121	AC007627	5	157000	F15F15	469663	17210	17217	IND	2	6/-6	
121	AC007627	5	157000	F15F15	469664	20385	20398	IND	2	12/-12	
121	AC007627	5	157000	F15F15	469665	22177	26936	IND	2	4758/-4758	
121	AC007627	5	157000	F15F15	469666	38443	38444	IND	2	-17/17	
121	AC007627	5	157000	F15F15	469667	38677	38690	IND	2	12/-12	
121	AC007627	5	157000	F15F15	469668	49697	49698	IND	2	-3/3	
121	AC007627	5	157000	F15F15	469669	49699	49700	IND	2	-3/3	
121	AC007627	5	157000	F15F15	469670	66767	66789	IND	2	21/-21	
121	AC007627	5	157000	F15F15	469671	70934	70940	IND	2	5/-5	
121	AC007627	5	157000	F15F15	469672	8497	8523	IND	2	25/-25	
121	AC007627	5	157000	F15F15	469673	8661	8662	IND	2	-14/14	
121	AC007627	5	157000	F15F15	469674	8665	8666	IND	2	-14/14	
121	AC007627	5	157000	F15F15	471147	86557	86558	IND	1	-2/2	
122	AP000418	5	16898	MPK17	470500	436	437	IND	2	-3/3	
123	AB028606	5	61510	F16F17	471938	51485	51487	SNP	1		G/A
123	AB028606	5	61510	F16F17	471939	51193	51195	SNP	1		G/A
123	AB028606	5	61510	F16F17	471940	51186	51188	SNP	1		G/A
123	AB028606	5	61510	F16F17	471941	51138	51140	SNP	1		G/A
123	AB028606	5	61510	F16F17	471942	51539	51541	SNP	1		A/G
123	AB028606	5	61510	F16F17	471943	51184	51186	SNP	1		A/G
123	AB028606	5	61510	F16F17	471944	51050	51052	SNP	1		C/T
123	AB028606	5	61510	F16F17	473070	60720	60722	SNP	1		C/A
123	AB028606	5	61510	F16F17	473071	60984	60986	SNP	1		C/A

Seq num	Seq id	Chromosome	BAC Length	BAC Name	Marker Name	Left	Right	Type	Method	Indel Size Columbia/ Landsberg	SNP Base Columbia/ Landsberg
123	AB028606	5	61510	F16F17	473072	60775	60777	SNP	1		G/C
123	AB028606	5	61510	F16F17	473073	61176	61178	SNP	1		C/T
124	AB028605	5	38089	F10E10	471929	36126	36128	SNP	1		T/A
124	AB028605	5	38089	F10E10	471930	36086	36088	SNP	1		T/A
124	AB028605	5	38089	F10E10	471931	36044	36046	SNP	1		T/G
124	AB028605	5	38089	F10E10	471932	36127	36129	SNP	1		A/T
124	AB028605	5	38089	F10E10	471933	36067	36069	SNP	1		G/T
124	AB028605	5	38089	F10E10	472117	26414	26416	SNP	1		G/A
124	AB028605	5	38089	F10E10	472118	26319	26321	SNP	1		G/A
124	AB028605	5	38089	F10E10	472119	26246	26248	SNP	1		A/C
124	AB028605	5	38089	F10E10	472120	26463	26465	SNP	1		A/T
124	AB028605	5	38089	F10E10	472434	33846	33848	SNP	1		T/A
124	AB028605	5	38089	F10E10	472550	103	105	SNP	1		G/A
124	AB028605	5	38089	F10E10	472551	157	159	SNP	1		T/A
124	AB028605	5	38089	F10E10	472552	381	383	SNP	1		G/A
124	AB028605	5	38089	F10E10	472553	718	720	SNP	1		T/A
124	AB028605	5	38089	F10E10	472554	151	153	SNP	1		A/C
124	AB028605	5	38089	F10E10	472555	362	364	SNP	1		A/G
124	AB028605	5	38089	F10E10	473085	16839	16841	SNP	1		A/G
124	AB028605	5	38089	F10E10	473089	14092	14094	SNP	1		A/T
124	AB028605	5	38089	F10E10	473444	1815	1817	SNP	1		T/A

Example 3

SNPs are identified by comparing *Arabidopsis thaliana,* Columbia and *Arabidopsis thaliana,* Landsberg *erecta* sequences. Each *Arabidopsis thaliana,* Columbia BAC sequence (extracted from GenBank and represented by a SEQ ID NO: 1 through SEQ ID NO: 124) is compared to a full set of *Arabidopsis thaliana,* Landsberg *erecta* contigs using WUBLAST (version 2.0) to locate areas of high identity that could contain a marker. Each identified contig is subsequently compared using WUBLAST to a full set of *Arabidopsis thaliana,* Columbia BACs (all of SEQ ID NO: 1 through SEQ ID NO: 124). To be selected as a marker candidate, an *Arabidopsis thaliana,* Landsberg *erecta* contig must have either one or two matches to an *Arabidopsis thaliana,* Columbia BAC. A single match suggests that that the sequence is unique. Two matches often result from overlapping BACs. The alignments are evaluated in a conservative manner. False negatives are preferable to false positives. To be included as a candidate polymorphic marker there must be: a minimum alignment of 200 bases between the sequence of an *Arabidopsis thaliana,* Landsberg *erecta* contig and the sequence of an *Arabidopsis thaliana,* Columbia BAC; the alignment must cover at least 75% of the length of the *Arabidopsis thaliana,* Landsberg *erecta* contig; a minimum of two reads of the *Arabidopsis thaliana,* Landsberg *erecta* region with the two read areas extending at least 25 bases on each side of the polymorphism position; agreement between all *Arabidopsis thaliana,* Landsberg *erecta* reads at the polymorphism position; minimum PHRAP consensus quality of 40 at the polymorphism position, with an average quality of 30 for the 25 bases on each side of the polymorphism position; and a maximum 1% polymorphism across the sequence. SNPs and INDELs of less than three nucleotide bases identified as described above are set forth in Table A.

A set of fifty polymorphisms was selected from among the polymorphisms in Table A.

Example 4

PCR primers can be designed for the flanking sequence of polymorphisms and can be used to either confirm or detect the polymorphisms. Such primers are designed with the program Primer3 (obtained from the MIT-Whitehead Genome Center) with a "perl-oracle" wrapper. The criteria applied to design a primer include:

Primer annealing temperature (minimum 57°C, optimum 60°C, maximum 63 °C)

Primer length (minimum 18 bp, optimum 20 bp, maximum 27 bp)

G+C content (minimum 20%, maximum 80%)

Minimum target margin of the primer relative to the polymorphism: 50 bp

Length of the amplified region
for SNPs: minimum 480 bp, optimum 500 bp, maximum 550 bp
for INDELs: minimum 200 bp, optimum 400 bp, maximum 500 bp

PHRED quality score of the gene template (minimum of 0)

Target sequence on one contig

Maximum mismatch = 12.0 (weighted score from Primer3 program)

Pair Max Misprime = 24.0 (weighted score from Primer3 program)

Maximum N's = 0

Maximum poly-X = 5

The primary goal of the design process is the creation of groups of primer pairs with a common annealing temperature (T_m).

After the *Arabidopsis thaliana* specific portion of the primers is selected, an additional common primer tail sequence can be added to the 5' ends. Forward primers for the detection of insertion/deletion polymorphisms have the additional common M13 bases on the 5' end: (5'-CAGCACGTTGTAAAACGAC-3'); reverse primers for the detection of insertion/deletion polymorphisms were designed without a tail. Forward primers for the detection of SNPs have the additional common M13 bases on the 5' end: (5'-TGTAAAACGACGGCCAGTT-3'); reverse primers for SNPs have the additional

common M13 bases on the 5' end: (5'-CAGGAAACAGCTATGACC-3'). The primer tail sequences are added so that subsequent amplifications of any primer pair can be done with a specific kit designed to work with oligonucleotides having the primer tail. It is noted that primer pairs are not required to contain the tail sequence, the relevant portion for amplification and/or hybridization probes being the *Arabidopsis thaliana* specific sequences.

Using such primers for polymorphic marker flanking sequence, a person skilled in the art can amplify genetic regions from *Arabidopsis thaliana,* Columbia and *Arabidopsis thaliana,* Landsberg *erecta* genomic DNA, as well as from a mixture of *Arabidopsis thaliana,* Columbia and *Arabidopsis thaliana,* Landsberg *erecta* genomic DNA to represent a heterozygote. In the case of SNPs the amplified product is purified and sequenced to confirm the presence of a predicted SNP. For validation of INDELs, the amplified products are analyzed or sized on an agarose gel or an acrylamide gel to determine if the fragments amplified from *Arabidopsis thaliana,* Columbia and *Arabidopsis thaliana,* Landsberg *erecta* genomic DNA are polymorphic. An exemplary PCR amplification reaction procedure to detect an INDEL-type polymorphism in a mapping experiment is a follows: a reaction mixture containing 4 ng/μl DNA (2.6μl); Taq Gold Polymerase (5 units/μl) (0.1μl) (Perkin Elmer, Norwalk, Connecticut); 5 μm forward and reverse primer (0.2μl); 1μm Li-Cor M13 Forward/IRD 700 (0.5μl)(Lincoln, Nebraska); 50 mM $MgCl_2$ (0.3μl); 10 mM dNTPs (2.5 mM each of dCTP, dGTP, dATP and dTTP)(0.8μl); 10X Taq Gold Buffer (1.0μl); dH_2O (4.5μl). Thermal amplification is carried out in an MJ Tetrad as follows: 94°C 10 minutes; 35 cycles (94°C 1 minute, 56°C 1 minute, 72°C 1 minute); 72°C 10 minutes; 4°C hold. PCR products are loaded on a 7% Long Ranger gel and run on Li-Cor's DNA Sequencer Long Redir 4200 or DNA Analyzer Gene Readir 4200 according to manufacturer's protocol. Data is analyzed using GeneImagIR software.

An exemplary PCR amplification reaction to detect a SNP-type polymorphism in a mapping experiment is a follows: A reaction mixture containing 4ng/μl DNA (6.6μl); 5 units Platinum Gold Polymerase (5 units/μl)(0.1μl) (GibcoBRL, Rockville, Maryland (0.11μl); 5 μm forward and reverse primer with M13 tails (1.39μl); 50 mM $MgCl_2$ (0.66μl); 10 mM dNTPs (2.5 mM each of dCTP, dGTP, dATP and dTTP)(1.04μl); 10X Taq Platinum Buffer (2.43μl); dH_2O (12.77μl). Thermal amplification is carried out in an MJ Tetrad as follows: 94°C 10 minutes; 35 cycles (94°C 1 minute, 56°C 1 minute, 72°C 1 minute); 72°C 10 minutes; 4°C hold. PCR products are purified using QIAGEN's QIAquick 96 PCR Purification Kit as per manufactures' protocol. Purified PCR products are run on agarose gels to confirm amplification, followed by sequencing to confirm the presences of a SNP.

We claim:

1. A method of isolating a region of genomic DNA associated with a phenotype of interest comprising:

(A) identifying an *Arabidopsis* plant of a first ecotype with a phenotype of interest;

(B) crossing said *Arabidopsis* plant with an *Arabidopsis* plant of a second ecotype lacking said phenotype;

(C) propagating and self pollinating seeds from said cross;

(D) selecting progeny of self pollinated seeds with said phenotype;

(E) screening progeny of self pollinated seeds with said phenotype with a collection of nucleic acid molecules, said collection of nucleic acid molecules capable of detecting a set of polymorphisms where the polymorphisms are distributed throughout the genome of said self pollinated seeds with said phenotype at an average density of more than one polymorphism per about 100kb, wherein at least one of the polymorphisms is selected from Table A;

(F) calculating the linkage of each of said polymorphisms to said phenotype; and

(G) isolating said region of genomic DNA associated with said phenotype based on its linkage to one or more of said nucleic acid molecules.

2. The method of isolating a region of genomic DNA associated with a phenotype of interest according to claim 1, wherein said region of genomic DNA associated with said phenotype is located between about 5 and about 10 cM of one or more of said polymorphisms.

3. The method of isolating a region of genomic DNA associated with a phenotype of interest according to claim 1, wherein said region of genomic DNA associated with said

phenotype is located between about 0 and about 5 cM of one or more of said polymorphisms.

4. A method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of nucleic acid molecules, wherein said nucleic acid molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb, wherein at least one of the polymorphisms is selected from Table A;

(B) calculating the linkage of each of said polymorphisms to said phenotypic trait; and

(C) identifying said genomic DNA region associated said phenotypic trait based on its linkage to one or more of said nucleic acid molecules.

5. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, further comprising isolating said identified region.

6. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 4, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 25 polymorphisms selected from Table A.

7. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 6, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 50 polymorphisms selected from Table A.

8. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 7, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 75 polymorphism selected from Table A.

9. The method of identifying a region of genomic DNA associated with a phenotypic trait of interest according to claim 8, wherein said collection of nucleic acid molecules is capable of detecting a set of greater than 100 polymorphisms selected from Table A.

10. A method of identifying a nucleic acid molecule associated with a phenotypic trait of interest comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of polymorphisms, wherein said polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an average density of more than one polymorphism per about 100kb, wherein at least one of the polymorphisms is selected from Table A;

(B) calculating the linkage of each of said polymorphism to said phenotypic trait; and

(C) isolating said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

11. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said collection of polymorphisms comprises at least 25 polymorphisms selected from Table A.

12. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 11, wherein said collection of polymorphisms comprises at least 50 polymorphisms selected from Table A.

13. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 12, wherein said collection of polymorphisms comprises at least 75 polymorphisms selected from Table A.

14. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 13, wherein said collection of polymorphisms comprises at least 100 polymorphisms selected from Table A.

15. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 5 and about 10 cM of one or more of said polymorphisms.

16. The method of identifying a nucleic acid molecule associated with a phenotypic trait of interest according to claim 15, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 0 and about 5 cM of one or more of said polymorphisms.

17. A method of isolating a nucleic acid molecule associated with a phenotypic trait comprising:

(A) screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of polymorphisms, wherein said at least one polymorphism is selected from Table A; and

(B) isolating said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

18. A collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population, wherein said collection of non-identical nucleic acid molecules is capable of detecting at least 25 polymorphisms selected from the group consisting of Table A.

19. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 18, wherein said collection non-identical nucleic acid molecules is capable of detecting at least 25 polymorphisms which are single nucleotide polymorphisms.

20. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 18, wherein said collection non-identical nucleic acid molecules is capable of detecting at least 25 polymorphisms are insertion or deletion polymorphisms.

21. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 518, wherein said collection of non-identical nucleic acid molecules is capable of detecting at least 50 polymorphisms selected from the group consisting of Table A.

22. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 21, wherein said collection of non-identical nucleic acid molecules is capable of detecting at least 100 polymorphisms selected from the group consisting of Table A.

23. The collection of non-identical nucleic acid molecules capable of detecting polymorphisms present in an *Arabidopsis* mapping population according to claim 18, wherein said collection of non-identical nucleic acid molecules is deposited on a substrate.

24. Computer readable medium having recorded thereon at least 100 of the polymorphisms set forth in Table A.

25. A method of introgressing a trait of interest into a plant comprising using a nucleic acid marker for marker assisted selection of said plant, said nucleic acid marker capable of detecting a polymorphism selected from Table A, and introgressing said trait into said plant.

26. A method for identifying transposons in the DNA of an organism comprising identifying INDELs in said DNA and comparing the sequence of said INDELs to the sequence of one or more known transposons.

Abstract

The present invention is in the field of plant genetics. More specifically, the invention relates to nucleic acid markers associated with *Arabidopsis thaliana* ecotypes. The invention also relates to methods for detecting polymorphisms. The invention further relates to methods of using nucleic acid markers, for example, for genome mapping, gene identification, gene isolation and gene analysis.